



(19)

Europäisches Patentamt

European Patent Office

Office européen des brevets



(11)

EP 0 791 655 A2

(12)

EUROPEAN PATENT APPLICATION

(43) Date of publication:
27.08.1997 Bulletin 1997/35

(51) Int Cl. 6: C12N 15/52, C12N 9/00,
C12N 15/63, C12P 17/08,
C12P 19/62

(21) Application number: 97301056.4

(22) Date of filing: 19.02.1997

(84) Designated Contracting States:
AT BE CH DE DK ES FI FR GB GR IE IT LI LU NL
PT SE

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(54) Polyketide synthase genes

(57) A DNA molecule isolated from *Streptomyces*

fradiae encodes the multi-functional proteins which direct the synthesis of the polyketide tylactone.

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Description

The present invention relates to DNA molecules responsible for encoding the multi-functional proteins that direct the biosynthesis of polyketide compounds, the products encoded by said DNA molecules, recombinant DNA expression vectors, and transformed microbial host cells.

Polyketides are a family of compounds that include a large number of structurally and functionally diverse natural products. For example, the polyketides provide the structural backbone for compounds that exhibit a variety of biological activities, such as, antibiotic, antitumor, and immunosuppressive agents.

Although the polyketides are quite diverse as indicated, they share a common mechanistic scheme of biosynthesis.

The polyketides are synthesized by the successive condensation of small carboxylic acid residues followed by variable reduction steps at the resulting β -keto carbon (i.e., β -carbonyl) moiety in a process that is similar to the synthesis of fatty acids. The iterative synthetic process for many of these polyketides is controlled by a complex of large, multi-functional polypeptides that have distinct sites for the variety of activities that are required.

The general scheme for polyketide biosynthesis has been reviewed, for example, in Hopwood and Sherman, Annu. Rev. Genet., 1990, 24:37 and Katz and Donadio, Annu. Rev. Microbiol., 1993, 47:875.

Naturally-occurring DNA sequences that encode the polyketide synthase enzymes have generally been found to be organized into repeated subunits, or modules, each of which encodes all the activities required in a single round of synthesis, which includes the condensation step itself and the post-condensation processing steps. Each activity is associated with a distinct site, which contributes to the specificity for the particular carboxylic acid building block that is incorporated at each condensation step, or which dictates the particular post-condensation processing functions that will be executed.

For example, PCT publication WO 93/13663 describes the organization of the gene encoding the polyketide synthase of *Saccharopolyspora erythraea*. The gene is organized in modules, with each module effecting one condensation step. The precise sequence of chain growth and the processing of the growing chain is determined by the genetic information in each module. This PCT application describes an approach for synthesizing novel polyketide structures by manipulating in several ways the DNA governing the biosynthesis of the cyclic lactone framework. In order to adapt this methodology to other polyketides, however, the DNA molecules directing the biosynthetic processing must first be isolated.

The present invention is directed to the DNA sequence for the gene cluster responsible for encoding tylactone synthase, the building machinery of tylactone, which is the basic building block of tylosin. As a result, the present invention enables modification of the DNA sequence so as to alter the type of carboxylic acids incorporated, the number of carboxylic acids incorporated, the post-condensation reactions performed, or any combination thereof, thereby resulting in novel tylosin-related polyketides.

The present invention provides a DNA molecule comprising an isolated DNA sequence that encodes a tylactone synthase domain. Thus, the present invention provides the DNA molecule of SEQ ID NO:1 and DNA molecules that contain submodules thereof. The present invention also provides the products encoded by said DNA molecules, recombinant DNA expression vectors, and transformed microbial host cells.

Figure 1 is a map of the tylactone polyketide synthase region (*tylG*) of the *Streptomyces fradiae* DNA (~45 kb). Distances in kb are relative to the beginning of *tylG*. Open reading frames (ORFs) are indicated by arrows. Restriction sites are denoted as follows:

E - *EcoRI*
B - *BamHI*

45 Predicted functional domains are labeled as follows:

ACP -	acyl carrier protein
AT -	acyltransferase
DH -	dehydratase
50 ER -	enoylreductase
KR -	ketoreductase
KR' -	ketoreductase-like domain predicted to be inactive
KS -	ketosynthase
KS' -	ketosynthase-like domain in which a glutamine residue is present in the position occupied by an active site cysteine in a normal ketosynthase
TE -	thioesterase.

Figure 2 depicts the biosynthetic pathway for tylactone synthesis.

Figure 3 is a map of the two clones that span the whole region of the *tylG* DNA.

Figure 4 is a map of the *srmG* region of the *Streptomyces ambofaciens* DNA. Distances in kb are relative to the beginning of *srmG*. Open reading frames are indicated by arrows. The *srmG* DNA (0-42 kb) is the platenolide polyketide synthase region. Restriction sites are denoted as above with additions as follows:

5	AP -	<i>Apal</i>
	G -	<i>BgII</i>
	K -	<i>KpnI</i>
	P -	<i>PstI</i>
10	X -	<i>XbaI</i>

Predicted functional domains are labeled as above.

Figure 5 demonstrates the biosynthetic pathway for platenolide synthesis.

Figure 6 is a map of the two clones that span the whole region of the *srmG* DNA.

15 Polyketides are a large class of structurally and functionally diverse natural products. A common feature of compounds in this class is that their synthesis is accomplished under the direction of a complex of multi-functional peptides, termed a "polyketide synthase." Molecular genetic analysis of polyketide synthase genes has revealed two distinct classes of enzymes operating for different polyketides: 1) the aromatics, which are made through an essentially iterative process, and 2) the complex polyketides, which comprise several repeats of the same activities arranged in few very

20 large polypeptides.

Among the complex polyketide synthase genes, a polyketide synthase includes enzymatic and regulatory activities responsible for exercising substrate specificity, catalyzing the condensation of small carboxylic acid building blocks (in the form of coenzyme A thioesters) to a growing polyketide carbon chain, and catalyzing the post-condensation processing reactions at the β -carbonyl functional group that results from the condensation reaction.

25 The condensation reaction requires several activities including acyl carrier protein (ACP), β -ketosynthase (KS), and acyltransferase (AT). Once a condensation has occurred, the resulting β -carbonyl functional group may be modified. Post-condensation activities that may be involved include β -ketoreductase (KR), dehydratase (DH), and enoylreductase (ER). Polyketide biosynthesis is terminated by a thioesterase (TE) activity. Whether all, some, or none of these activities act after a particular condensation step determines the structure of the final product.

30 The present invention provides, in particular, the DNA sequence encoding the polyketide synthase responsible for biosynthesis of tylactone, i.e., tylactone synthase. Tylactone itself is the polyketide backbone of the commercially significant antibiotic tylosin. The tylactone synthase DNA sequence, which defines the tylactone synthase gene cluster, directs biosynthesis of the tylactone polyketide by encoding the various distinct activities of tylactone synthase.

35 The gene cluster for tylactone synthase, like other complex polyketide biosynthetic genes whose organization has been elucidated, is characterized by the presence of several open reading frames (ORFs), each of which contains one or more repeated units termed "modules." A module is defined as the genetic element encoding all of the distinct activities required in a single round of synthesis, i.e., one condensation step and all the β -carbonyl processing steps associated therewith. Each module encodes an ACP, a KS, and an AT activity to accomplish the condensation portion of the synthesis, and selected post-condensation activities to effect β -carbonyl processing. The polypeptides encoded by such modules are termed "synthase units" (SUs).

40 Each module is further characterized by the inclusion of submodules that are responsible for encoding the distinct activities of tylactone synthase. For purposes of the present invention, the term "submodule" is defined as the portion of the polyketide synthase DNA sequence that encodes a distinct activity, or "domain". Thus, a domain is taken as commonly understood to mean that part of the polyketide synthase polypeptide necessary for a given distinct activity.

45 Organization of the tylactone synthase gene cluster derived from *Streptomyces fradiae*, is shown in Figure 1. The tylactone synthetic pathway, with indications of the specific carboxylic acid substrates used for each condensation reaction and the various post-condensation activities, is shown in Figure 2.

50 A preferred DNA molecule comprising the tylactone synthase gene cluster isolated from *Streptomyces fradiae* is represented by SEQ ID NO:1. Other preferred DNA molecules of the present invention include the various open reading frames of SEQ ID NO:1 that encode individual multi-functional polypeptides. These are represented by the following nucleotide residues of SEQ ID NO:1: ORF1 816 to 14234, ORF2 14351 to 19945, ORF3 20010 to 31199, ORF4 31232 to 36067, and ORF5 36249 to 41774. The predicted amino acid sequences of the various peptides encoded by these sequences are shown in SEQ ID NO:2, 3, 4, 5, and 6, respectively.

55 Yet other preferred DNA molecules of the present invention include the modules that encode the synthase units, which include all the activities necessary for a single round of synthesis. These are represented by the following nucleotide residues of SEQ ID NO:1: Starter Module 942 to 3929, Module 1 3993 to 8471, Module 2 8541 to 13970, Module 3 14411 to 19666, Module 4 20136 to 24611, Module 5 24675 to 30902, Module 6 31337 to 35743, and Module 7 36360 to 40826. The predicted amino acid sequences of the various synthase units encoded by these modules are

represented, respectively, by the following amino acid residues: Starter SU 43 to 1038, SU1 1060 to 2552 and SU2 2576 to 4385 in SEQ ID NO:2; SU3 21 to 1772 in SEQ ID NO:3; SU4 43 to 1534 and SU5 1556 to 3631 in SEQ ID NO:4; SU6 36 to 1504 in SEQ ID NO:5; and SU7 38 to 1526 in SEQ ID NO:6.

Still other preferred DNA molecules include the various submodules that encode the various domains of tylactone synthase. These submodules are represented by the following nucleotide residues: KS^Q(s) 942 to 2156, AT(s) 2571 to 3557, ACP(s) 3675 to 3929, KS1 3993 to 5264, AT1 5631 to 6617, KR1 7410 to 7949, and ACP1 8220 to 8471 of Module 1 in SEQ ID NO:1; KS2 8541 to 9812, AT2 10260 to 11246, DH2 11319 to 11876, KR2 12861 to 13415, and ACP2 13719 to 13970 of Module 2 in SEQ ID NO:1; KS3 14411 to 15697, AT3 16055 to 17122, DH3 17198 to 17794, KR3 18584 to 19138, and ACP3 19415 to 19666 of Module 3 in SEQ ID NO:1; KS4 20136 to 21404, AT4 21771 to 22757, KR4 23541 to 24077, and ACP4 24360 to 24611 of Module 4 in SEQ ID NO:1; KS5 24675 to 25949, AT5 26292 to 27284, DH5 27360 to 27917, ER5 28767 to 29813, KR5 29829 to 30368, and ACP5 30651 to 30902 of Module 5 in SEQ ID NO:1; KS6 31337 to 32608, AT6 32975 to 33961, KR6 34694 to 35236, and ACP6 35492 to 35743 of Module 6 in SEQ ID NO:1; KS7 36360 to 37631, AT7 37989 to 38987, KR7 39759 to 40313, ACP7 40575 to 40826, and TE7 41235 to 41333 of Module 7 in SEQ ID NO:1.

The predicted amino acid sequences of the various domains encoded by these submodules are represented, respectively, by KS^Q(s) 43 to 447, AT(s) 586 to 914, ACP(s) 954 to 1038, KS1 1060 to 1483, AT1 1606 to 1934, KR1 2199 to 2378, and ACP1 2469 to 2552 in SEQ ID NO:2; KS2 2576 to 2999, AT2 3149 to 3477, DH2 3502 to 3687, KR2 4016 to 4200, and ACP2 4302 to 4385 in SEQ ID NO:2; KS3 21 to 449, AT3 569 to 924, DH3 950 to 1148, KR3 1412 to 1596, and ACP3 1689 to 1772 in SEQ ID NO:3; KS4 43 to 465, AT4 588 to 916, KR4 1178 to 1356, and ACP4 1451 to 1534 in SEQ ID NO:4; KS5 1556 to 1980, AT5 2095 to 2425, DH5 2451 to 2636, KR5 3274 to 3453, and ACP5 3548 to 3631 in SEQ ID NO:4; KS6 36 to 459, AT6 582 to 910, KR6 1155 to 1335, and ACP6 1421 to 1504 in SEQ ID NO:5; KS7 38 to 461, AT7 581 to 913, KR7 1171 to 1355, ACP7 1443 to 1526, and TE7 1663 to 1695 in SEQ ID NO:6.

Although not wishing to be bound to any particular technical explanation, sequence similarity exists among domain boundaries in various polyketide synthase genes. Thus, one skilled in the art is able to predict the domain boundaries of newly discovered polyketide synthase genes based on the sequence information of known polyketide synthase genes. In particular, the boundaries of submodules, domains, and open reading frames in the instant application are predicted based on sequence information disclosed in the instant application and the locations of the domain boundaries of the erythromycin polyketide synthase (Donadio et al., Gene 111:51 (1992)).

The DNA sequence of the tylactone synthase gene was determined from recombinant DNA clones prepared from the DNA of *Streptomyces fradiae*. The tylactone synthase gene is contained in recombinant DNA vectors pSET506 and pSET507 (Figure 3), which are available from the National Center for Agricultural Utilization Research, 1815 North University Street, Peoria, Illinois 61604-3999, in *E. coli* K12 MM294 under accession numbers NRRL B-18688 (deposited July 19, 1990) and NRRL B-18689 (deposited July 19, 1990), respectively.

Techniques for isolating bacterial DNA are readily available and well known in the art. Any such technique can be employed in this invention. In particular, DNA from these cultures is isolated as follows. Lyophils of *E. coli* K12 MM294/pSET506 or *E. coli* K12 MM294/pSET507 are plated onto L-agar (10 g tryptone, 10 g NaCl, 5 g yeast extract, and 15 g agar per liter) plates containing 100 µg/ml ampicillin to obtain a single colony isolate of the strain. This colony is used to inoculate about 500 ml of L-broth (10 g tryptone, 10 g NaCl, 5 g yeast extract per liter) containing 100 µg/ml ampicillin, and the resulting culture is incubated at 37° C with aeration until the cells reach stationary phase. Cosmid DNA is obtained from the cells in accordance with procedures known in the art (see e.g., Rao et al., 1987 in Methods in Enzymology, 153:166).

DNA of the current invention can be sequenced using any known techniques in the art such as the dideoxynucleotide chain-termination method (Sanger, et al., Proc. Natl. Acad. Sci. 74:5463 (1977)) with either radioisotopic or fluorescent labels. Double-stranded, supercoiled DNA was used directly for templates in sequence reactions with sequence-specific oligonucleotide primers. Alternatively, fragments were used to prepare libraries of either random, overlapping sequences in the bacteriophage M13 or nested, overlapping deletions in a plasmid vector. Individual recombinant DNA subclones were then sequenced with vector-specific oligonucleotide primers. Radioactive reaction products were electrophoresed on denaturing polyacrylamide gels and analyzed by autoradiography. Fluorescent-labeled reaction products were electrophoresed and analyzed on Applied Biosystems (ABI Division, Perkin Elmer, Foster City, CA 94404) model 370A and 373A or DuPont (Wilmington, DE) Genesis DNA sequencers. Sequence data was assembled and edited using Genetic Center Group (GCG, Madison, WI) programs GelAssemble and SeqEd or the ABI model 670 Inherit Sequence Analysis system and the AutoAssembler and SeqEd programs.

Polypeptides corresponding to a domain, a synthase unit, or a multi-functional polypeptide can be produced by expression of the cDNA sequence in a bacteria, for example, using known expression vectors. Alternatively, the polypeptides mentioned above can be extracted from tylactone-producing bacteria such as *Streptomyces fradiae*. In addition, the techniques of synthetic chemistry can be employed to synthesize the polypeptides mentioned above. The procedures and techniques for isolation and purification of homogenous protein or polypeptides are well known in the art.

Since the genetic organization of the tylactone synthase gene cluster appears to correspond to the order of the reactions required to complete synthesis of tylactone, knowledge of the tylactone synthase DNA sequence, its genetic organization, and the activities associated with particular open reading frames, modules, and submodules of the gene enables production of novel polyketides having a predicted structure that are not otherwise available. Modifications 5 may be made to the DNA sequence that either alter the initial carboxylic acid building block used or the building block added at any of the condensation steps. The tylactone synthase gene may also be modified to alter the actual number of condensation steps done, thereby changing the size of the carbon backbone. Modifications to portions of the DNA sequence that encode the post-condensation processing activities will alter the functional groups appearing at the various condensation sites on the carbon chain backbone.

10 These modifications can be accomplished by substituting submodules derived from the tylactone synthase gene and having known activities for corresponding submodules from another polyketide synthase gene having different activities. Submodules from tylactone synthase may also be combined with submodules from other polyketide synthase genes to effect additional catalytic steps. Accordingly, a DNA molecule wherein at least one submodule from the tylactone synthase gene has been combined with, or substituted for, submodules from the DNA sequence of other 15 polyketide synthase genes is also provided by the present invention. Further, submodules that are a part of the present invention may be selectively inactivated thereby giving rise to predictable novel polyketide structures.

For example, a submodule encoding a KS' activity, an AT activity, and an ACP activity, all derived from the first 20 open reading frame of the tylactone synthase gene (ORF1), were exchanged for the corresponding submodule in the platenolide synthase gene (see Example 2). Platenolide is the polyketide backbone of the antibiotic spiramycin.

The submodule from the tylactone synthase gene encodes a domain that catalyzes the incorporation of a propionate 25 as the initial building block whereas the corresponding submodule of the platenolide synthase gene encodes a domain that catalyzes the incorporation of an acetate building block. When the resulting DNA molecule was placed into a bacterial strain and grown under conditions promoting polyketide synthesis, a hybrid molecule having the structure that would be predicted by incorporation of an additional methyl side-chain at the start of the growing polyketide chain was synthesized, in particular, 16-methyl platenolide.

One skilled in the art is fully familiar with the degeneracy of the genetic code. Consequently, the skilled artisan can 30 modify the specific DNA sequences provided by this disclosure to provide proteins having the same or improved characteristics compared to those polypeptides specifically provided herein. Also, one skilled in the art can modify the DNA sequences to express an identical protein to those provided, albeit expressed at higher levels. Furthermore, one skilled 35 in the art is familiar with means to prepare synthetically, either partially, or in whole, DNA sequences which would be useful in preparing recombinant DNA vectors or coding sequences which are encompassed by the current invention. Additionally, recombinant means for modifying the DNA sequences provided may include for example site-directed deletion or site-directed mutagenesis. These techniques are well known to those skilled in the art and require no further elaboration here. Consequently, as used herein, DNA which is isolated from natural sources, prepared synthetically or semi-synthetically, or which are modified by recombinant DNA methods, are within the scope of the present invention.

Likewise, those skilled in the art will recognize that the polypeptides of the invention may be expressed recombinantly. Alternatively, these polypeptides may be synthesized as well, either in whole or in part, by conventional known 40 non-recombinant techniques; for example, solid-phase synthesis. Thus, the present invention should not be construed as necessarily limited to any specific vector constructions or means for production of the specific polyketide synthase molecules exemplified. These alternate means for preparing the present polypeptides are meant to be encompassed by the present invention.

Many cyclized polyketides undergo glycosylation at one or more sites. Tylosin is a 16-membered cyclic lactone, tylactone, with three attached sugar residues. The process of converting tylactone to tylosin is well known in the art. The present invention also provides the information needed to synthesize novel tylosin-related polyketides based on 45 tylactone. The principles have already been described above. In addition, any product resulting from post-transcriptional or post-translational modification *in vivo* or *in vitro* based on the DNA sequence information disclosed herein are meant to be encompassed by the present invention.

The following examples are provided for exemplification purposes only and are not intended to limit the scope of the invention which has been described in broad terms above.

50 EXAMPLE 1

The DNA sequence of the *Streptomyces fradiae* tylactone synthase gene, *tylG*, was obtained by sequencing the inserts of recombinant DNA subclones containing contiguous or overlapping DNA segments, which when considered 55 cumulatively span the entire region of *tylG*. All sequences representing *tylG* are fully contained in the overlapping cosmid subclones pSET506 and pSET507.

In accord with the current invention, the sequence may now be obtained by subcloning and sequencing the DNA fragment designated by EcoRI restriction sites at 3.0 and 4.0 kb on the map presented in Figure 3, the fragment bounded

by the *Eco*RI site at 4.0 kb and the *Bam*HI site at 7.5 kb, the fragments bounded by *Bam*HI sites at 7.5, 12.0, 23.4, 27.3, 34.6, 39.5, and 50.5 kb.

In order to obtain the *tylG* gene on a single DNA fragment, the 31.6 kb DNA fragment bounded by the *Eco*RI site at 3.0 kb and the *Bam*HI site at 34.6 kb is isolated from a partial digestion of pSET506 with the restriction enzymes *Eco*RI and *Bam*HI. The 15.9 kb DNA fragment bounded by the *Bam*HI sites at 34.6 and 50.5 kb is isolated from a partial digestion of pSET507 with the restriction enzyme *Bam*HI. The resulting fragments are ligated and cloned in an appropriate recombinant DNA vector. Clones containing the correct orientation of the two ligated fragments are identified by restriction enzyme site mapping.

10 EXAMPLE 2

Production of a polyketide hybrid of platenolide and tylactone

The lactone rings of the polyketides platenolide and tylactone undergo an identical set of post-condensation processing steps. However, these two polyketides are synthesized by condensation of more than one type of carboxylic acid and the specific building blocks chosen for incorporation in the two pathways differ. The organization of the platenolide gene cluster is shown in Figure 4 along with the accompanying synthetic pathway in Figure 5. The specific carboxylic acid substrates that are used for each condensation reaction and the post-condensation activities of platenolide synthesis are indicated.

20 The DNA sequence of the *Streptomyces ambofaciens* platenolide synthase (*srmG*) genes was obtained by sequencing inserts of recombinant DNA subclones containing contiguous or overlapping DNA segments, which when considered together span the entire *srmG* region. All sequences representing *srmG* are fully contained in the overlapping cosmid clones pKC1080 and pKC1306 (Figure 6). The sequence can be obtained by subcloning and sequencing the fragments bounded by *Nru*I sites at position 1, 0.3 kb, 8.2 kb, 14.1 kb, 20.2 kb, 29.5 kb, 31.4 kb, 41.1 kb, and 42.0 kb.

25 In order to obtain the *srmG* region on a single fragment, the 25.0 kb fragment bounded by the *Nru*I site at position 1 and the *Sfu*I site at 25.0 kb is isolated from a partial digestion of pKC1080 with restriction enzymes *Nru*I and *Sfu*I. The 17.8 kb DNA fragment bounded by the *Sfu*I sites at 25.0 kb and 42.8 kb is isolated by digestion of pKC1306 with the restriction enzyme *Sfu*I. The resulting fragments are ligated and cloned in an appropriate recombinant DNA vector. Clones containing the correct orientation of the two ligated fragments are identified by restriction enzyme mapping.

30 An exchange of tylactone polyketide synthase DNA with corresponding platenolide DNA was effected as follows in order to generate a novel polyketide structure.

A strain of *Streptomyces ambofaciens*, the organism that produces platenolide, was constructed with most of ORF1 deleted. This ORF1-deficient strain produced no detectable platenolide. To confirm that the lack of ORF1 was the only deficiency in platenolide production, a construct containing ORF1, and not any functional activities of ORFs 2-5, was introduced into the ORF1-deficient strain on a vector that contains the site-specific integration function from the streptomycete phage φC31. Integration of ORF1 at the φC31 *att* site restored spiramycin production to parental levels, confirming that ORF1 codes for a functional protein and that ORFs 2-5 are expressed in the ORF1-deficient strain.

35 ORF1 of *tylG* is organized like *srmGORF1*. DNA coding for a KS', an AT, and an ACP from *tylORF1* was exchanged with the corresponding region from *srm ORF1* by replacing an *Eco*RI-*Apal* fragment of *srm ORF1* with an *Eco*RI-*Sfu*I fragment from *tylORF1*, generating plasmid pKC1524. When pKC1524 was introduced into the ORF1-deficient strain, polyketide synthesis was restored. The products produced by this restored strain were indistinguishable from those produced by the parental strain of *Streptomyces ambofaciens* when analyzed by thin-layer chromatography and HPLC.

40 The hybrid ORF1 DNA sequence is SEQ ID NO:7 and the amino acid sequence of the ORF1-encoded polypeptide is SEQ ID NO:8. The rest of the DNA sequence of the hybrid molecule is identical to original *tylG* sequence and the polypeptides encoded by this remaining portion are therefore identical as well.

45 In order to simplify physical analysis of the putative novel polyketide, an *Xba*I fragment encoding sugar synthesis or addition was deleted from the restored. Deletion of this fragment led to a strain that produced only the lactone without any sugar residues added. When analyzed by NMR and mass spectroscopy, the isolated product made by this sugar-deficient strain was confirmed as 16-methylplatenolide, which is the structure that would be predicted from the incorporation of a propionate in place of the acetate normally utilized in platenolide synthesis.

SEQUENCE LISTING

5

10

(1) GENERAL INFORMATION:

15

- (i) APPLICANT: ELI LILLY AND COMPANY
(B) STREET: Lilly Corporate Center
(C) CITY: Indianapolis
(D) STATE: Indiana
(E) COUNTRY: United States of America
(F) ZIP: 46285

20

- (ii) TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES

- (iii) NUMBER OF SEQUENCES: 15

25

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- (A) ADDRESSEE: K. G. TAPPING
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(E) COUNTRY: United Kingdom
(F) ZIP: GU20 6PH

30

- (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Macintosh
(C) OPERATING SYSTEM: Macintosh 7.0
(D) SOFTWARE: Microsoft Word 5.1

35

40

(2) INFORMATION FOR SEQ ID NO:1:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

55

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 816..14234

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 14351..19945

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 20010..31199

5 (ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 31232..36067

10 (ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 36249..41774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15	GAATTCCGGG TCCGCTCGGG TTCCGGTCCG TTTCTGCTT CCAGCGTCTG TGTCCGTCATC	60
	TCGGCTCTCT CATCGGGCTG GTGCGGGAAG GCATCCCGGT GCGGGGAGAC ATCCTGCTGC	120
	GGGAAGGAAT CCTGGTGCAG GAAGGCAACG ACTGCGGGAC GCGGGAGAAA GGGGAATCGG	180
20	CGGGAATTTC CCCCAGCGGG CGGGGACGGT GCCGGAGAAC AACGGGGGG AAACAGCCCCG	240
	CGGTCCGTGA CGACAACCGA AACTATGGTC CGCTTCCTCC GTCCACAAAG CGAACCTGA	300
	CATACTCCCC CCCACGCGG AAATCCCGCA CGGCGGCCCG CGGGCCGCCG CACCGGACCT	360
25	GACATAGCCT CGCCGGACCG CTCCGGTGCG GCCACCCCGT TGGTGTGCG TGATGAGGTA	420
	CCGGATCAGA GGAGAAAGCA CCATGCCCCG CCCCTCGGCC AGCGAACCGC GCGGGACCAC	480
30	CCGTTCCGGCG ACCCGCGCTGG CGCGCCGCCG TGGACCGGGC CGTAACTCCC CTGCGCCATC	540
	GAATACTTCG CCCCTCGAAT CCCTCACCGG GCGAGTTCCA GGACCGCCCC TCGCTCTCGC	600
	CATACCGGAG AACGAACCCG AACGGCACCG CGGAAAGCCC GTCCGCAATG CCCGGGACAT	660
35	TCCCTGTGACC CGACAACACG GTTTGCCGAC ACGGTTGCC CGAACGCTTG TTGGCAGGCT	720
	CACCGGCACG GCCCGCTGAC ACAGCTCGGT GACACGGCAG CCTGACGGGA AACCGCCGAA	780
	GCCTCTGGAG TCCTCGCACA TTCCGGAGAG AACAG GTG TCT TCC GCG CTG CGG	833
40	Met Ser Ser Ala Leu Arg 1 5	
	CGC GCG GTG CAA TCC AAC TGT GGC TAC GGA GAC CTC ATG ACC TCG AAC	881
	Arg Ala Val Gln Ser Asn Cys Gly Tyr Gly Asp Leu Met Thr Ser Asn	
45	10 15 20	
	ACC GCT GCA CAG AAC ACC GGC GAC CAG GAA GAC GTC GAC GGT CCC GAC	929
	Thr Ala Ala Gln Asn Thr Gly Asp Gln Glu Asp Val Asp Gly Pro Asp	
	25 30 35	
50	AGC ACA CAC GGT GGG GAG ATC GCC GTC GTG GGA ATG TCG TGC CGT CTG	977
	Ser Thr His Gly Gly Glu Ile Ala Val Val Gly Met Ser Cys Arg Leu	
	40 45 50	
	CCG GGC GCG GCC GGT GTC GAG GAA TTC TGG GAA CTG CTG CGC AGC GGA	1025
55	Pro Gly Ala Ala Gly Val Glu Glu Phe Trp Glu Leu Leu Arg Ser Gly	
	55 60 65 70	

	CGC GGT ATG CCC ACC CGT CAG GAC GGC ACC TGG CCG GCC CCC CTG Arg Gly Met Pro Thr Arg Gln Asp Asp Gly Thr Trp Arg Ala Ala Leu 75 80 85	1073
5	GAG GAC CAC GCC CCC TTC GAC GCC GGG TTC TTC GGC ATG AAC GCC CGG Glu Asp His Ala Gly Phe Asp Ala Gly Phe Phe Gly Met Asn Ala Arg 90 95 100	1121
10	CAG GCC GCC ACC GAC CCG CAG CAC CGA CTG ATG CTG GAA CTC CGA Gln Ala Ala Ala Thr Asp Pro Gln His Arg Leu Met Leu Glu Leu Gly 105 110 115	1169
15	TGG GAG GCA CTG GAG GAC GCG GGC ATC GTC CCC GGC GAT CTC ACC CGC Trp Glu Ala Leu Glu Asp Ala Gly Ile Val Pro Gly Asp Leu Thr Gly 120 125 130	1217
20	ACC GAC ACC GGA GTC TTC GCC GGC GTG GCG TCC GAC GAC TAT GCC GTT Thr Asp Thr Gly Val Phe Ala Gly Val Ala Ser Asp Asp Tyr Ala Val 135 140 145 150	1265
25	CTC ACC CGC CGT TCC GCC GTC TCC GCC GGG GGA TAC ACC GCC ACG GGG Leu Thr Arg Arg Ser Ala Val Ser Ala Gly Gly Tyr Thr Ala Thr Gly 155 160 165	1313
30	CTG CAC CGC GCC CTG GCC GCC AAC CGC CTC TCC CAC TTC CTG GGC CTG Leu His Arg Ala Leu Ala Ala Asn Arg Leu Ser His Phe Leu Gly Leu 170 175 180	1361
35	CGC GGC CCC AGC CTG GTC GTC GAC TCG GCC CAG TCC GCC TCA CTG GTG Arg Gly Pro Ser Leu Val Val Asp Ser Ala Gln Ser Ala Ser Leu Val 185 190 195	1409
40	GCC GTC CAG CTC GCC TGC GAG AGT CTG CGC CGG GGT GAG ACG TCG CTC Ala Val Gln Leu Ala Cys Glu Ser Leu Arg Arg Gly Glu Thr Ser Leu 200 205 210	1457
45	GCC GTC GCG GGC GGT GTC AAC CTC ATC CTC ACC GAG GAG AGC ACC ACC Ala Val Ala Gly Gly Val Asn Leu Ile Leu Thr Glu Glu Ser Thr Thr 215 220 225 230	1505
50	GTC ATG GAG CGT ATG GGA GCG CTC TCA CCC GAC GGC CGC TGC CAC ACC Val Met Glu Arg Met Gly Ala Leu Ser Pro Asp Gly Arg Cys His Thr 235 240 245	1553
55	TTC GAC GCC CGC GCC AAC GGC TAC GTA CGC GGC GAG GGC GGC GGA GCC Phe Asp Ala Arg Ala Asn Gly Tyr Val Arg Gly Glu Gly Gly Ala 250 255 260	1601
	GTC GTG CTC AAG CCA CTG GAC GCC GCA CTC GCC GAC GGC GAC CGC GTG Val Val Leu Lys Pro Leu Asp Ala Ala Leu Ala Asp Gly Asp Arg Val 265 270 275	1649
	TAC TGC GTC ATC AAG GGA GGT GCC GTC AAC AAC GAC GGC GGC GGC GCG Tyr Cys Val Ile Lys Gly Gly Ala Val Asn Asn Asp Gly Gly Gly Ala 280 285 290	1697
	AGC CTC ACC ACT CCC GAC CGG GAG GCG CAG GAA GCT GTG CTG CGC CAG Ser Leu Thr Thr Pro Asp Arg Glu Ala Gln Glu Ala Val Leu Arg Gln 295 300 305 310	1745

EP 0 791 655 A2

	GCC TAC CGG CGG GCG GGC GTC AGC ACC GGC GCC GTC CGC TAC GTC GAG Ala Tyr Arg Arg Ala Gly Val Ser Thr Gly Ala Val Arg Tyr Val Glu 315 320 325	1793
5	CTG CAC GGG ACC GGC ACC CGG GCC GGC GAC CCC GTC GAG GCG GCC GCA Leu His Gly Thr Gly Thr Arg Ala Gly Asp Pro Val Glu Ala Ala Ala 330 335 340	1841
10	CTG GGC GCC GTG CTC GGG GCG GGG GCG GAC AGC GGC CGC AGC ACG CCG Leu Gly Ala Val Leu Gly Ala Gly Ala Asp Ser Gly Arg Ser Thr Pro 345 350 355	1889
15	CTC GCC GTC GGC TCG GTG AAG ACC AAC GTC GGC CAT CTG GAG GGC GCG Leu Ala Val Gly Ser Val Lys Thr Asn Val Gly His Leu Glu Gly Ala 360 365 370	1937
20	GCG GGC ATC GTC GGA CTG ATC AAG GCC ACG CTG TGC GTA CGG AAG GGC Ala Gly Ile Val Gly Leu Ile Lys Ala Thr Leu Cys Val Arg Lys Gly 375 380 385 390	1985
25	GAA CTC GTC CCC AGC CTC AAC TTC AGC ACG CCG AAC CCT GAC ATC CCC Glu Leu Val Pro Ser Leu Asn Phe Ser Thr Pro Asn Pro Asp Ile Pro 395 400 405	2033
30	CTC GAC GAC CTG CGG CTG CGC GTC CAG ACC GAA CGG CAG GAG TGG AAC Leu Asp Asp Leu Arg Leu Arg Val Gln Thr Glu Arg Gln Glu Trp Asn 410 415 420	2081
35	GAG GAG GAC GAC CGG CCG CGC GTG GCC GGC GTC TCC TCC TTC GGT ATG Glu Glu Asp Asp Arg Pro Arg Val Ala Gly Val Ser Ser Phe Gly Met 425 430 435	2129
40	GCC GGA ACC AAT GTC CAC CTC GTG ATC GCG GAG GCT CCG GCC GCG GCG Gly Gly Thr Asn Val His Leu Val Ile Ala Glu Ala Pro Ala Ala Ala 440 445 450	2177
45	GGG TCC TCC CGG CGG GGG GGT TCG GGC GCT GGT TCC GGT GCC GGT ATC Gly Ser Ser Gly Ala Gly Ser Gly Ala Gly Ser Gly Ala Gly Ile 455 460 465 470	2225
50	AGC GCT GTT TCT CGT GTG CCG GTG GTG GTT TCG GGG CGT TCG CCG Ser Ala Val Ser Gly Val Val Pro Val Val Ser Gly Arg Ser Arg 475 480 485	2273
55	GTG GTG GTG CGG GAG GCT GCG GGC CGG TTG GCG GAG GTG GTG GAG GCC Val Val Val Arg Glu Ala Ala Gly Arg Leu Ala Glu Val Val Glu Ala 490 495 500	2321
60	GGT GGT GTG GGG CTG GCG GAT GTG GCG GTG ACG ATG GCG GAC CGG TCG Gly Gly Val Gly Leu Ala Asp Val Ala Val Thr Met Ala Asp Arg Ser 505 510 515	2369
65	CGG TTT GGG TAT CGG GCG GTT GTG CTG GCT CGG GGT GAG GCT GAG CTT Arg Phe Gly Tyr Arg Ala Val Val Leu Ala Arg Gly Glu Ala Glu Leu 520 525 530	2417
70	GCC GGG CGT TTG CGG GCG TTG GCG GGG GGT GAT CCG GAC GCG GGT GTG Ala Gly Arg Leu Arg Ala Leu Ala Gly Gly Asp Pro Asp Ala Gly Val 535 540 545 550	2465

	GTC ACC GGT GCG GTT CTC GAC GGT GGT GTG GTT GTC GGT GCT GCC CCC Val Thr Gly Ala Val Leu Asp Gly Gly Val Val Val Gly Ala Ala Pro 555 560 565	2513
5	GCC GGT GCC GGT GCT GCC GGT GGT GCC GGT GCT GCC GGT GGT GCC GGT Gly Gly Ala Gly Ala Ala Gly Gly Ala Gly Ala Ala Gly Gly Ala Gly 570 575 580	2561
10	GGT GGG GGC GTG GTG TTG GTT TTC CCT GGT CAG GGG ACG CAG TGG GTG Gly Gly Gly Val Val Leu Val Phe Pro Gly Gln Gly Thr Gln Trp Val 585 590 595	2609
15	GGG ATG GGT GCG GCG CTG CTG GGG TCT TCG GAG GTG TTT GCG GCG TCG Gly Met Gly Ala Gly Leu Leu Gly Ser Ser Glu Val Phe Ala Ala Ser 600 605 610	2657
20	ATG CGG GAG TGT GCG CGG GCG CTG AGT GTT CAT GTG GGG TGG GAT TTG Met Arg Glu Cys Ala Arg Ala Leu Ser Val His Val Gly Trp Asp Leu 615 620 625 630	2705
25	CTG GAG GTG GTG TCG GGC GGG GCC GGG TTG GAG CGG GTG GAT GTG GTG Leu Glu Val Val Ser Gly Gly Ala Gly Leu Glu Arg Val Asp Val Val 635 640 645	2753
30	CAG CCG GTG ACG TGG GCG GTG ATG GTG TCG CTG GCC CGG TAC TGG CAG Gln Pro Val Thr Trp Ala Val Met Val Ser Leu Ala Arg Tyr Trp Gln 650 655 660	2801
35	GCG ATG GGT GTG GAC GTG GCT GCG GTG GTG GGT CAT TCC CAG GGG GAG Ala Met Gly Val Asp Val Ala Ala Val Val Gly His Ser Gln Gly Glu 665 670 675	2849
40	ATC GCC GCT GCC ACG GTG GCG GGG GCG TTG TCG CTG GAG GAT GCG GCG Ile Ala Ala Ala Thr Val Ala Gly Ala Leu Ser Leu Glu Asp Ala Ala 680 685 690	2897
45	GCT GTG GTC GCT CTG CGG GCG GGG TTG ATT GGC CGG TAT CTG GCG GGT Ala Val Val Ala Leu Arg Ala Gly Leu Ile Gly Arg Tyr Leu Ala Gly 695 700 705 710	2945
50	CGT GGT GCG ATG GCG GCT GTT CCG CTG CCT GCC CGG GAG GTC GAG GCG Arg Gly Ala Met Ala Ala Val Pro Leu Pro Ala Gly Glu Val Glu Ala 715 720 725	2993
55	GGG CTG GCG AAG TGG CCG GGT GTG GAG GTC GCG GCG GTC AAC GGT CCG Gly Leu Ala Lys Trp Pro Gly Val Glu Val Ala Ala Val Asn Gly Pro 730 735 740	3041
	GCG TCT ACG GTG GTT TCC GGG GAT CGG CGG GCG GTC GGC GGT TAT GTG Ala Ser Thr Val Val Ser Gly Asp Arg Arg Ala Val Ala Gly Tyr Val 745 750 755	3089
	GCC GTC TGT CAG GCG GAG GGT GTG CAG GCC CGG TTG ATA CCG GTG GAC Ala Val Cys Gln Ala Glu Gly Val Gln Ala Arg Leu Ile Pro Val Asp 760 765 770	3137
	TAC GCC TCT CAC TCC CGC CAT GTG GAG GAC CTG AAG GGC GAG TTG GAG Tyr Ala Ser His Ser Arg His Val Glu Asp Leu Lys Gly Glu Leu Glu 775 780 785 790	3185

	CGG GTG CTG TCC GGT ATC CGC CCC CGC AGT CCG CGG GTG CCG GTG TGT Arg Val Leu Ser Gly Ile Arg Pro Arg Ser Pro Arg Val Pro Val Cys 795 800 805	3233
5	TCC ACC GTC GCC GGA GAG CAG CCG GGC GAG CCG GTT TTC GAT GCG GGG Ser Thr Val Ala Gly Glu Gln Pro Gly Glu Pro Val Phe Asp Ala Gly 810 815 820	3281
10	TAT TGG TTC CGT AAT CTG CGG AAC CGG GTT GAG TTC TCC GCG GTG GTC Tyr Trp Phe Arg Asn Leu Arg Asn Arg Val Glu Phe Ser Ala Val Val 825 830 835	3329
15	GGT GGT TTG TTG GAG GAG GGC CAC CGT CGG TTC ATC GAG GTC AGT GCC Gly Gly Leu Leu Glu Glu His Arg Arg Phe Ile Glu Val Ser Ala 840 845 850	3377
20	CAC CCG GTA CTC GTC CAT GCG ATC GAG CAG ACG GCC GAG GCC GCG GAC His Pro Val Leu Val His Ala Ile Glu Gln Thr Ala Glu Ala Ala Asp 855 860 865 870	3425
25	CGG AGT GTC CAT GCC ACC GGG ACC CTG CGC CGC CAG GAC GAC AGC CCG Arg Ser Val His Ala Thr Gly Thr Leu Arg Arg Gln Asp Asp Ser Pro 875 880 885	3473
30	CAC CGC CTG CTG ACC TCC ACC GCC GAG GCC TGG GCC CAC GGC GCC ACC His Arg Leu Leu Thr Ser Thr Ala Glu Ala Trp Ala His Gly Ala Thr 890 895 900	3521
35	CTC ACC TGG GAC CCC GCC CTG CCC CCA GGC CAC CTC ACC ACC CTC CCC Leu Thr Trp Asp Pro Ala Leu Pro Pro Gly His Leu Thr Thr Leu Pro 905 910 915	3569
40	ACC TAC CCC TTC AAC CAC CAC TAC TGG CTC GAC ACC ATT GAC GGG Thr Tyr Pro Phe Asn His His Tyr Trp Leu Asp Thr Ile Asp Gly 920 925 930	3617
45	GGC GGA GGG GAC GCG ACC CAG GAG AAG GAG AGC GGC CCT CTG ACG Gly Gly Gly Asp Asp Ala Thr Gln Glu Lys Glu Ser Gly Pro Leu Thr 935 940 945 950	3665
50	CGG GAA CTG CGT GGG CTG CCG TCC TCT CAG AAG CAA CTG GGT TTC CTG Arg Glu Leu Arg Gly Leu Pro Ser Ser Gln Lys Gln Leu Gly Phe Leu 955 960 965	3713
55	CTC GAT CTG GTG TGC CGG CAC ACG GCC GTC GTA CTC GGC CTG GAC ACG Leu Asp Leu Val Cys Arg His Thr Ala Val Val Leu Gly Leu Asp Thr 970 975 980	3761
60	GCC GCC GAG GTG GAC CCG GAC CTG TCC TTC AAG AAG CAG GGC ATC CAG Ala Ala Glu Val Asp Pro Asp Leu Ser Phe Lys Lys Gln Gly Ile Gln 985 990 995	3809
65	TCC ATG ACC GGC GTC GAG CTG CGC AAC AGG CTG CTG ACC GAG ACC GGC Ser Met Thr Gly Val Glu Leu Arg Asn Arg Leu Leu Thr Glu Thr Gly 1000 1005 1010	3857
70	CTG GCA TTG CCC ACC ACC CTC GTC TAC GAC CGG CCC ACC CCT CGC GCC Leu Ala Leu Pro Thr Thr Leu Val Tyr Asp Arg Pro Thr Pro Arg Ala 1015 1020 1025 1030	3905

	CTG GCG CAG TTC CTC CAC ACC GAG TTG CTC GAC GGC TCC CCC TCG GGC Leu Ala Gln Phe Leu His Thr Glu Leu Leu Asp Gly Ser Pro Ser Gly 1035 1040 1045	3953
5	TCC GTC CTC GCA CCG GCG CAG AAG AGC TTC GAA GCC CAG GAG CCG ATC Ser Val Leu Ala Pro Ala Gln Lys Ser Phe Glu Ala Gln Glu Pro Ile 1050 1055 1060	4001
10	CCG GTG GTG CGT ATG CGG TGC CGG TTC CCC GGT GGG GTG GGT TCG CCG Ala Val Val Gly Met Gly Cys Arg Phe Pro Gly Gly Val Gly Ser Pro 1065 1070 1075	4049
15	GAG GCG TTG TGG CGG TTG GTG GTG GAG GGG GTG GAC GCG GTT TCC CCG Glu Ala Leu Trp Arg Leu Val Val Glu Gly Val Asp Ala Val Ser Pro 1080 1085 1090	4097
20	TTT CCC GGT GAT CGT GGC TGG GAT GTG GAG GGG TTG TAC GAC CCG GAG Phe Pro Gly Asp Arg Gly Trp Asp Val Glu Gly Leu Tyr Asp Pro Glu 1095 1100 1105 1110	4145
25	CCG GGT GTG CCG GGG AAG TCG TAT GTG CGG GAG GGG GGT TTT CTG CAT Pro Gly Val Ala Gly Lys Ser Tyr Val Arg Glu Gly Phe Leu His 1115 1120 1125	4193
30	GAT GCG GCG GAG TTC GAT GCG GAG TTC TTC GGG ATT TCG CCG CGT GAG Asp Ala Ala Glu Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg Glu 1130 1135 1140	4241
35	GGC GTG GCG ATG GAT CCG CAG CAG CGG CTG TTG CTG GAG ACC TCC TGG Ala Val Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr Ser Trp 1145 1150 1155	4289
40	GAG GCG ATC GAG CGG GCG GGT ATC GAC CCG CAC TCG CTG CAC GGC AGC Glu Ala Ile Glu Arg Ala Gly Ile Asp Pro His Ser Leu His Gly Ser 1160 1165 1170	4337
45	CGC ACC GGC GTC TAC GCC GGC GTG ATG CCG CAG GAA TAC GGA CCT CGG Arg Thr Gly Val Tyr Ala Gly Val Met Pro Gln Glu Tyr Gly Pro Arg 1175 1180 1185 1190	4385
50	CTC GCC GAA GGA GCG GAA GGC AGC GAC GGC TAC CTC CTC ACC GGT ACG Leu Ala Glu Gly Ala Glu Gly Ser Asp Gly Tyr Leu Leu Thr Gly Thr 1195 1200 1205	4433
55	TCG GGG AGT GTG GTG TCG GGG CGT GTG GCC TAC ACG CTG GGG CTG GAG Ser Gly Ser Val Val Ser Gly Arg Val Ala Tyr Thr Leu Gly Leu Glu 1210 1215 1220	4481
	GGT CCG GCC GTG ACC GTG GAT ACG GCG TGT TCG TCG TCG TTG GTG GCG Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser Leu Val Ala 1225 1230 1235	4529
	TTG CAT CTG GCG GTG CAG GCG TTG CGG GGT GGC GAG TGT GAC ATG GCG Leu His Leu Ala Val Gln Ala Leu Arg Gly Gly Glu Cys Asp Met Ala 1240 1245 1250	4577
	TTG GCC GGT GGT GTG ACG GTG ATG GCC GGG CCG GGG ATG TTC GTG GAG Leu Ala Gly Gly Val Thr Val Met Ala Gly Pro Gly Met Phe Val Glu 1255 1260 1265 1270	4625

	TTT TCG CCG CAG CGG GGG TTG GCG GCC GAT GGG CGG TGC AAG GCG TTC Phe Ser Arg Gln Arg Gly Leu Ala Ala Asp Gly Arg Cys Lys Ala Phe 1275 1280 1285	4673
5	GCG GAT GGG GCG GAT GGG ACC GCT TGG GCC GAG GGT GCG GGG GTG GTG Ala Asp Gly Ala Asp Gly Thr Ala Trp Ala Glu Gly Ala Gly Val Val 1290 1295 1300	4721
10	CTG CTG GAG CGG TTG TCG GAT GCC CGG CGG TTG GGG CAT CCG GTG TTG Leu Val Glu Arg Leu Ser Asp Ala Arg Arg Leu Gly His Pro Val Leu 1305 1310 1315	4769
15	GCG GTG GTG TGT GGG TCG GCG GTG AAT CAG GAC GGT GCG TCG AAT GGT Ala Val Val Cys Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly 1320 1325 1330	4817
	TTG ACG CCC CCG AGT GGT CCG TCG CAG GAG CGG GTG ATT CGT CAG GCG Leu Thr Ala Pro Ser Gly Pro Ser Gln Glu Arg Val Ile Arg Gln Ala 1335 1340 1345 1350	4865
20	TTG CGG AAT GCG CGG TTG ACG GTG GCG GAT GTG GAT GTG GTG GAG GCG Leu Gly Asn Ala Arg Leu Thr Val Ala Asp Val Asp Val Val Glu Ala 1355 1360 1365	4913
25	CAT GGG ACG GGG ACG CGG CTG CGT GAT CCG ATC GAG GCG CAG GCG TTG His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu 1370 1375 1380	4961
30	CTG GGG ACG TAT GGG CGG GAT CGT GAT CGT GGG CGT CCG GTG TGG TTG Leu Gly Thr Tyr Gly Arg Asp Arg Gly Arg Pro Val Trp Leu 1385 1390 1395	5009
	GGG TCG TTG AAG TCG AAT ATT GGT CAT GCT CAG GCG GCT GCG GGG GTG Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln Ala Ala Ala Gly Val 1400 1405 1410	5057
35	GCT GGT GTG ATC AAG ATG GTG TTG GCG ATG CGG TAT GGG TGG TTG CCG Ala Gly Val Ile Lys Met Val Leu Ala Met Arg Tyr Gly Trp Leu Pro 1415 1420 1425 1430	5105
40	CGG ACG TTG CAT GTC GAT GAG CCG AGC CGG CAT GTG GAC TGG TCG GCT Arg Thr Leu His Val Asp Glu Pro Ser Arg His Val Asp Trp Ser Ala 1435 1440 1445	5153
	GGT GGT GTG TGG TTG CTG ACC GAG GCG CGG GAG TGG CCG GGG GTG GAC Gly Gly Val Trp Leu Leu Thr Glu Ala Arg Glu Trp Pro Gly Val Asp 1450 1455 1460	5201
45	CGG CCG CGT CGG GCG GTC TCC GCC TTT GGT GTC AGT GGT ACC AAC Arg Pro Arg Arg Ala Ala Val Ser Ala Phe Gly Val Ser Gly Thr Asn 1465 1470 1475	5249
50	GCC CAT CTG ATC CTC GAA GCC CCC GAC ACC GCC GAG GCG GAG AGC GCC Ala His Leu Ile Leu Glu Ala Pro Asp Thr Ala Glu Ala Glu Ser Ala 1480 1485 1490	5297
55	ACG ACC CCG GTC CGC TCT GAG GTG TCG GAG TCT GCT GCG GTC CTC GAT Thr Thr Pro Val Arg Ser Glu Val Ser Glu Ser Ala Ala Val Leu Asp 1495 1500 1505 1510	5345

	GCC CGC AGT GGT GTG GTG CCG GTG GTG GTT TCG GGG CGT TCG CGG GTG Ala Arg Ser Gly Val Val Pro Val Val Val Ser Gly Arg Ser Arg Val 1515 1520 1525	5393
5	GTG GTG CGG GAG GCT GCG GGC CGG TTG GCG GAG GTG GTG GAG GCC GGT Val Val Arg Glu Ala Ala Gly Arg Leu Ala Glu Val Val Glu Ala Gly 1530 1535 1540	5441
10	CGT GTG CGG CTG GCG GAT GTG GCG GTG ACG ATG GCG GGC CGG TCG CGG Gly Val Gly Leu Ala Asp Val Ala Val Thr Met Ala Gly Arg Ser Arg 1545 1550 1555	5489
15	TTT GGG TAT CGG GCG GTT GTG CTG GCT CGG GGT GAG GCT GAG CTT GCC Phe Gly Tyr Arg Ala Val Val Leu Ala Arg Gly Glu Ala Glu Leu Ala 1560 1565 1570	5537
20	GGG CGT TTG CGG GCG TTG GCG GGG GGT GAT CCG GAC GCG GCG GGT GTG GTC Gly Arg Leu Arg Ala Leu Ala Gly Gly Asp Pro Asp Ala Gly Val Val 1575 1580 1585 1590	5585
25	ACC GGT GCG GTG GTG GAC CCG GAG ACG GGG TCC GGT GGT GGG GGC GTG Thr Gly Ala Val Val Asp Pro Glu Thr Gly Ser Gly Gly Gly Val 1595 1600 1605	5633
30	GTG TTG GTT TTC CCT GGT CAG GGG ACG CAG TGG GTG GGG ATG GGT GCG Val Leu Val Phe Pro Gly Gln Gly Thr Gln Trp Val Gly Met Gly Ala 1610 1615 1620	5681
35	GGG CTG CTG GGG TCT TCG GAG GTG TTT GCG GCG TCG ATG CGG GAG TGT Gly Leu Leu Gly Ser Ser Glu Val Phe Ala Ala Ser Met Arg Glu Cys 1625 1630 1635	5729
40	GCG CGG GCG CTG AGT GTT CAT GTG GAG TGG GAT TTG CTG GAG GTG GTG Ala Arg Ala Leu Ser Val His Val Glu Trp Asp Leu Leu Glu Val Val 1640 1645 1650	5777
45	TCG GGC GGG GCC GGG TTG GAG CGG GTG GAT GTG GTG CAG CCC GTG ACG Ser Gly Gly Ala Gly Leu Glu Arg Val Asp Val Val Gln Pro Val Thr 1655 1660 1665 1670	5825
50	TGG GCG GTG ATG GTG TCG CTG GCC CGG TAC TGG CAG GCG ATG GGT GTG Trp Ala Val Met Val Ser Leu Ala Arg Tyr Trp Gln Ala Met Gly Val 1675 1680 1685	5873
55	GAC GTG GCT GCG GTG GTG GGT CAT TCC CAG GGG GAG ATC GCT GCT GCC Asp Val Ala Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala 1690 1695 1700	5921
	ACG GTG GCG GGG GCG TTG TCG CTG GAG GAT GCG GCG GCT GTG GTC GCT Thr Val Ala Gly Ala Leu Ser Leu Glu Asp Ala Ala Val Val Ala 1705 1710 1715	5969
	CTG CGG GCG GGG TTG ATT GGC CGG TAT CTG GCG GGT CGT GGT GCG ATG Leu Arg Ala Gly Leu Ile Gly Arg Tyr Leu Ala Gly Arg Gly Ala Met 1720 1725 1730	6017
	GCG GCT GTT CCG CTG CCT GCC GGC GAG GTC GAG GCC GGG CTG GCG AAG Ala Ala Val Pro Leu Pro Ala Gly Glu Val Glu Ala Gly Leu Ala Lys 1735 1740 1745 1750	6065

	TGG CCG GGT GTG GAG GTC GCG GCG GTC AAC GGT CCG GCG TCC ACG GTG Trp Pro Gly Val Glu Val Ala Ala Val Asn Gly Pro Ala Ser Thr Val 1755 1760 1765	6113
5	GTT TCC GGG GAT CGG CGG GCG GTG GCC GGT TAT GTG GCC GTC TGT CAG Val Ser Gly Asp Arg Arg Ala Val Ala Gly Tyr Val Ala Val Cys Gln 1770 1775 1780	6161
10	GCG GAG GGT GTG CAG GCT CGG TTG ATA CCG GTG GAC TAC GCC TCT CAC Ala Glu Gly Val Gln Ala Arg Leu Ile Pro Val Asp Tyr Ala Ser His 1785 1790 1795	6209
15	TCC CGC CAT GTG GAG GAC CTG AAG GGC GAG TTG GAG CGG GTG CTG TCC Ser Arg His Val Glu Asp Leu Lys Gly Glu Leu Glu Arg Val Leu Ser 1800 1805 1810	6257
	GGT ATC CGC CCC CGC AGT CCG CGG GTG CCG GTG TGT TCC ACC GTC GCC Gly Ile Arg Pro Arg Ser Pro Arg Val Pro Val Cys Ser Thr Val Ala 1815 1820 1825 1830	6305
20	GGA GAG CAG CCG GGC GAG CCG GTT TTC GAT GCG GGG TAT TGG TTC CGT Gly Glu Gln Pro Gly Glu Pro Val Phe Asp Ala Gly Tyr Trp Phe Arg 1835 1840 1845	6353
25	AAT CTG CGG AAC CGG GTT GAG TTC TCC GCG GTG GTC GGT GGT TTG TTG Asn Leu Arg Asn Arg Val Glu Phe Ser Ala Val Val Gly Gly Leu Leu 1850 1855 1860	6401
30	GAG GAG GGC CAC CGT CGG TTC ATC GAG GTC AGT GCC CAC CCG GTA CTC Glu Glu Gly His Arg Arg Phe Ile Glu Val Ser Ala His Pro Val Leu 1865 1870 1875	6449
	GTC CAT GCG ATC GAG CAG ACG GCC GAG GCG GAC CGG AGT GTC CAT Val His Ala Ile Glu Gln Thr Ala Glu Ala Ala Asp Arg Ser Val His 1880 1885 1890	6497
35	GCC ACC GGG ACC CTG CGC CGC CAG GAC GAC AGC CCG CAC CGC CTG CTG Ala Thr Gly Thr Leu Arg Arg Gln Asp Asp Ser Pro His Arg Leu Leu 1895 1900 1905 1910	6545
40	ACC TCC ACC GCC GAG GCC TGG GCC CAC GGC GCC ACC CTC ACC TGG GAC Thr Ser Thr Ala Glu Ala Trp Ala His Gly Ala Thr Leu Thr Trp Asp 1915 1920 1925	6593
	CCC GCC CTG CCC CCA GGC CAC CTC ACC ACC CTC CCC ACC TAC CCC TTC Pro Ala Leu Pro Pro Gly His Leu Thr Thr Leu Pro Thr Tyr Pro Phe 1930 1935 1940	6641
45	AAC CAC CAC CAC TAC TGG CTC GAC ACC ACC CCC ACC ACC CCC GCG ACG Asn His His His Tyr Trp Leu Asp Thr Thr Pro Thr Thr Pro Ala Thr 1945 1950 1955	6689
50	ACC ACC CAG AGC CCC ACC GAT GCC TGG CGC TAC CGC GTC ACC TGG AAA Thr Thr Gln Ser Pro Thr Asp Ala Trp Arg Tyr Arg Val Thr Trp Lys 1960 1965 1970	6737
55	GCC CTG ACC GAA TCC TCC CCC GTC CGC CCT CAC TCC ATC GGT CGC TGC Ala Leu Thr Glu Ser Ser Pro Val Arg Pro His Ser Ile Gly Arg Cys 1975 1980 1985 1990	6785

	CTC CTC GTT GCA CCC CCG ACC ACC GAC GGC GAG CTC CTC GAC GGA CTG Leu Leu Val Ala Pro Pro Thr Thr Asp Gly Glu Leu Leu Asp Gly Leu 1995 2000 2005	6833
5	ACA ACG GTG TTG TCC GAG CGC GGT GCC TCC GTC GCC CGC CTT GAG GTG Thr Thr Val Leu Ser Glu Arg Gly Ala Ser Val Ala Arg Leu Glu Val 2010 2015 2020	6881
10	CCC ATC GGC GCG CGG CGT GCC GAG GTC GCC GAA CTG CTC AAG CCC TCC Pro Ile Gly Ala Arg Arg Ala Glu Val Ala Glu Leu Leu Lys Pro Ser 2025 2030 2035	6929
15	ATG GAG TCA GCG GGG GAG GAG AAC ACC ACC GTC GTC TCG CTT CTC GGT Met Glu Ser Ala Gly Glu Glu Asn Thr Thr Val Val Ser Leu Leu Gly 2040 2045 2050	6977
20	CTG GTG CCC TCC ACG GAC GCG GTC AGG ACG TCG ATA GCG CTC CTC CAG Leu Val Pro Ser Thr Asp Ala Val Arg Thr Ser Ile Ala Leu Leu Gln 2055 2060 2065 2070	7025
25	GCG GTC TCC GAC ATC GGC GTC CCG GCC AGG GTC TGG GCG CTG ACG Ala Val Ser Asp Ile Gly Val Pro Ala Ala Arg Val Trp Ala Leu Thr 2075 2080 2085	7073
30	CGG AGG GCC GTG GCC GTG GTT CCC GGG GAG ACG CCG CAG GAC GCG GGG Arg Arg Ala Val Ala Val Val Pro Gly Glu Thr Pro Gln Asp Ala Gly 2090 2095 2100	7121
35	GCC CAG TTG TGG GGC TTC GGA CGA GTG GCG GCC CTT GAA CTC CCG GAT Ala Gln Leu Trp Gly Phe Gly Arg Val Ala Ala Leu Glu Leu Pro Asp 2110 2115	7169
40	ATC TGG GGC GGC TTG ATC GAT CTG CCG GAG ACA GCG GAG CTG ACG CGG Ile Trp Gly Gly Leu Ile Asp Leu Pro Glu Thr Ala Glu Leu Thr Arg 2120 2125 2130	7217
45	ACG CCG GAG ACC TCA CAG CCC CCA CAG ACC CCG GAG AGG CTG CCG CAG Thr Pro Glu Thr Ser Gln Pro Pro Gln Thr Pro Glu Arg Leu Pro Gln 2135 2140 2145 2150	7265
50	ACT CCG AAC CGA CGC GCC CTT GAG CTT GCT GCC GCC GTC CTC GCC GGC Thr Pro Asn Arg Arg Ala Leu Glu Leu Ala Ala Ala Val Leu Ala Gly 2155 2160 2165	7313
55	CGC GAC GGC GAG GAC CAG GTC GCC GTG CGC GCC TCG GGG ATC TAC GGG Arg Asp Gly Glu Asp Gln Val Ala Val Arg Ala Ser Gly Ile Tyr Gly 2170 2175 2180	7361
	CGG CGG GTG TCG CGG GCC GCG GCA GCG GGG GCC GCC TCC TGG CAG CCG Arg Arg Val Ser Arg Ala Ala Ala Gly Ala Ala Ser Trp Gln Pro 2185 2190 2195	7409
	TCC GGC ACG GTG CTG ATC ACC GGC GGC ATG GGT GCC ATC GGC AGG CGG Ser Gly Thr Val Leu Ile Thr Gly Gly Met Gly Ala Ile Gly Arg Arg 2200 2205 2210	7457
	CTC GCC CGC AGG CTG GCG GCC GAG GGA GCC GAA CGC CTG GTC CTC ACC Leu Ala Arg Arg Leu Ala Ala Glu Gly Ala Glu Arg Leu Val Leu Thr 2215 2220 2225 2230	7505

	AGC CGT CGC GGA CCG GAG GCG CCG GGC GCC GCC GAA CTC GCC GAG GAA Ser Arg Arg Gly Pro Glu Ala Pro Gly Ala Ala Glu Leu Ala Glu Glu 2235 2240 2245	7553
5	CTG CGA GGA CAT GGC TGC GAG GTC GTG CAC GCG GCC TGT GAC GTG GCC Leu Arg Gly His Gly Cys Glu Val Val His Ala Ala Cys Asp Val Ala 2250 2255 2260	7601
10	GAG CGT GAT GCG CTC GCC GCG CTC GTC ACC GCG TAT CCG CCG AAC GCC Glu Arg Asp Ala Leu Ala Ala Leu Val Thr Ala Tyr Pro Pro Asn Ala 2265 2270 2275	7649
15	GTC TTC CAC ACC GCC GGG ATT CTG GAC GAC GCG GTG ATC GAC ACG CTG Val Phe His Thr Ala Gly Ile Leu Asp Asp Ala Val Ile Asp Thr Leu 2280 2285 2290	7697
20	TCA CCG GAG AGC TTC GAG ACC GTC CGC GGG GCG AAG GTG TGC GGC GCG Ser Pro Glu Ser Phe Glu Thr Val Arg Gly Ala Lys Val Cys Gly Ala 2295 2300 2305 2310	7745
25	GAG CTG CTG CAC CAA CTG ACT GCG GAC ATA AAA GGG TTG GAC GCC TTC Glu Leu Leu His Gln Leu Thr Ala Asp Ile Lys Gly Leu Asp Ala Phe 2315 2320 2325	7793
30	GTC CTC TTC TCC TCC GTC ACC GGC ACA TGG GGC AAC GCC GGC CAG GGT Val Leu Phe Ser Ser Val Thr Gly Thr Trp Gly Asn Ala Gly Gln Gly 2330 2335 2340	7841
35	GCG TAC GCC GCC AAC GCC GCG CTC GAC GCC CTC GCC GAG CGT CGC Ala Tyr Ala Ala Asn Ala Ala Leu Asp Ala Leu Ala Glu Arg Arg 2345 2350 2355	7889
40	CGT GCC GCC GGA CTG CCC GCG ACC TCC GTC GCC TGG GGC CTT TGG GGC Arg Ala Ala Gly Leu Pro Ala Thr Ser Val Ala Trp Gly Leu Trp Gly 2360 2365 2370	7937
45	GGG GGA GGC ATG GCG GCG GGT GCG GGC GAG GAG AGT CTG TCG CGG CGA Gly Gly Gly Met Ala Ala Gly Ala Gly Glu Glu Ser Leu Ser Arg Arg 2375 2380 2385 2390	7985
50	GGG CTG CGG GCC ATG GAC CCC GAC GCG GCC GTC GAC GCG CTC CTG GGC Gly Leu Arg Ala Met Asp Pro Asp Ala Ala Val Asp Ala Leu Leu Gly 2395 2400 2405	8033
55	GCC ATG GGC AGG AAC GAC GTG TGC GTC ACT GTC GTC GAC GTC GAC TGG Ala Met Gly Arg Asn Asp Val Cys Val Thr Val Val Asp Val Asp Trp 2410 2415 2420	8081
	GAG CGT TTC GCG CCC GCG ACG AAC GCC ATC CGT CCC GGG CGG CTG TTC Glu Arg Phe Ala Pro Ala Thr Asn Ala Ile Arg Pro Gly Arg Leu Phe 2425 2430 2435	8129
	GAC ACC GTG CCG GAG GCG CGG GAG GCC CTG ACG GCA GCC GGC ACC ACG Asp Thr Val Pro Glu Ala Arg Glu Ala Leu Thr Ala Ala Gly Thr Thr 2440 2445 2450	8177
	TCC GCG ACG CCG GAC GCG CCC GAG CTG GCG CGG CGG TTG TCC ATG Ser Ala Thr Pro Asp Gly Ala Pro Glu Leu Ala Arg Arg Leu Ser Met 2455 2460 2465 2470	8225

	CTG AAC GAG ACC GAA CGC CTG CCG AAG CTG GTC GAA CTC GTC CGT ACC Leu Asn Glu Thr Glu Arg Leu Arg Lys Leu Val Glu Leu Val Arg Thr 2475 2480 2485	8273
5	GAG GCG GCC TTT GTG CTG CCG CAT CCG AAC ACG GAC GCC ATC GGC GCC Glu Ala Ala Phe Val Leu Arg His Pro Asn Thr Asp Ala Ile Gly Ala 2490 2495 2500	8321
10	GAA CGC CCG TTC AAG TCG GCC GGT TTC GAC TCC CTG ACC TCC CTG GAA Glu Arg Pro Phe Lys Ser Ala Gly Phe Asp Ser Leu Thr Ser Leu Glu 2505 2510 2515	8369
15	CTC CGC AAC CGC CTC AAT GCC GGC ACA GGC CTG AAG CTA CCC GCC ACC Leu Arg Asn Arg Leu Asn Ala Gly Thr Gly Leu Lys Leu Pro Ala Thr 2520 2525 2530	8417
20	GTC ATC TTC GAC CAC CCC ACC CCG ACC GCC CTG GCC AGA CTG CTG CTC Val Ile Phe Asp His Pro Ser Pro Thr Ala Leu Ala Arg Leu Leu Leu 2535 2540 2545 2550	8465
25	GAC CGG CTG ACC GGC GGC GGA GCC CCC GCG CCC GCC GGC GAT GAG CCG Asp Arg Leu Thr Gly Ala Gly Ala Pro Ala Pro Ala Ala Asp Glu Pro 2555 2560 2565	8513
30	CCA CTG CCC GTC GCC GTG GCC GAC GAC CCG GTG GTC ATC GTC GGC Pro Leu Pro Val Ala Val Ala Asp Asp Asp Pro Val Val Ile Val Gly 2570 2575 2580	8561
35	ATG GCG TGC CGT TTC CCC GGT GGG GCG GGC ACC CCT GAG GCG CTG TGG Met Ala Cys Arg Phe Pro Gly Gly Ala Gly Thr Pro Glu Ala Leu Trp 2585 2590 2595	8609
40	AAG CTG GTG ACC GAG GAG CGT GAC GTC ATA GGC GCC GCG CCC ACC GAC Lys Leu Val Thr Glu Glu Arg Asp Val Ile Gly Ala Ala Pro Thr Asp 2600 2605 2610	8657
45	CGG GGC TGG GAC CTG GAT TCC GTC TAC GAC CCG GAG CCG GGT GTG GCG Arg Gly Trp Asp Leu Asp Ser Val Tyr Asp Pro Glu Pro Gly Val Ala 2615 2620 2625 2630	8705
50	GGG AAG ACA TAT GTG CGG GAG GGG GGT TTT CTC CAC GAC GCG GCG GAG Gly Lys Thr Tyr Val Arg Glu Gly Gly Phe Leu His Asp Ala Ala Glu 2635 2640 2645	8753
55	TTC GAC GCG GAG TTC TTC GGG ATT TCG CCG CGT GAG GCG GCG GTG GCG ATG Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg Glu Ala Val Ala Met 2650 2655 2660	8801
	GAT CCG CAG CAG CGG CTG TTG CTG GAG ACC TCC TGG GAG GCG ATC GAG Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr Ser Trp Glu Ala Ile Glu 2665 2670 2675	8849
	CGG GCG GGT ATC GAC CCG CAC TCG CTG CAC GGC AGC CGC ACC GGG GTA Arg Ala Gly Ile Asp Pro His Ser Leu His Gly Ser Arg Thr Gly Val 2680 2685 2690	8897
	TAC GTC GGG CTG ACC CAT CAG GAG TAC GCC TCC CGG CTG CAC GAG GCC Tyr Val Gly Leu Thr His Gln Glu Tyr Ala Ser Arg Leu His Glu Ala 2695 2700 2705 2710	8945

	CCG GAG GAG TAC GAA GGC TAT CTG CTC ACC GGC AAG TCG GCG AGC GTC Pro Glu Glu Tyr Glu Gly Tyr Leu Leu Thr Gly Lys Ser Ala Ser Val 2715 2720 2725	8993
5	GTC TCC GGC CGC ATC TCG TAC ACG CTG GGG CTG GAG GGT CCT TCG CTC Val Ser Gly Arg Ile Ser Tyr Thr Leu Gly Leu Glu Gly Pro Ser Leu 2730 2735 2740	9041
10	TCC ATC GAC ACC GCG TGT TCG TCG CTG GTC GCC CTG CAC AAC GCG Ser Ile Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His Asn Ala 2745 2750 2755	9089
15	GCG CAG GCG TTG CGG GGT GGC GAG TGT GAC ATG GCG TTG GCC GGT GGT Ala Gln Ala Leu Arg Gly Gly Glu Cys Asp Met Ala Leu Ala Gly Gly 2760 2765 2770	9137
20	GTG ACG GTG ATG GCG GCA CCC GGA TTG TTC GTG GAG TTT TCG CGG CAG Val Thr Val Met Ala Ala Pro Gly Leu Phe Val Glu Phe Ser Arg Gln 2775 2780 2785 2790	9185
25	CGG GGG TTG GCG GCC GAT GGG CGG TGC AAG GCG TTC GCG GAT GGG GCG Arg Gly Leu Ala Ala Asp Gly Arg Cys Lys Ala Phe Ala Asp Gly Ala 2795 2800 2805	9233
30	GAT GGG ACC GCT TGG GCC GAG GGT GCG GGG GTG GTG CTG GTG GAG CGG Asp Gly Thr Ala Trp Ala Glu Gly Ala Gly Val Val Leu Val Glu Arg 2810 2815 2820	9281
35	TTG TCG GAT GCC CGG CGG TTG GGG CAT CCG GTG TTG GCG GTG GTG TGT Leu Ser Asp Ala Arg Arg Leu Gly His Pro Val Leu Ala Val Val Cys 2825 2830 2835	9329
40	GGG TCG GCG GTG AAT CAG GAC GGT GCG TCG AAT GGT TTG ACG GCG CCG Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro 2840 2845 2850	9377
45	AGT GGT CCG TCG CAG GAG CGG GTG ATT CGT CAG GCG TTG GCG AAT GCG Ser Gly Pro Ser Gln Glu Arg Val Ile Arg Gln Ala Leu Ala Asn Ala 2855 2860 2865 2870	9425
50	CGG TTG ACG GTG GCG GAT GTG GAT GTG GTG GAG GCG CAT GGG ACG GGG Arg Leu Thr Val Ala Asp Val Asp Val Val Glu Ala His Gly Thr Gly 2875 2880 2885	9473
55	ACG CGG CTG GGT GAT CCG ATC GAG GCG CAG GCG TTG CTG GGG ACG TAT Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Leu Gly Thr Tyr 2890 2895 2900	9521
	GGG CGG GAT CGT GAT GCT GAG TGT CCG GTG TGG TTG GGG TCG TTG AAG Gly Arg Asp Arg Asp Ala Glu Cys Pro Val Trp Leu Gly Ser Leu Lys 2905 2910 2915	9569
	TCG AAT ATT GGT CAT GCT CAG GCG GCT GCG GGG GTG GCT GGT GTG ATC Ser Asn Ile Gly His Ala Gln Ala Ala Gly Val Ala Gly Val Ile 2920 2925 2930	9617
	AAG ATG GTG TTG GCG ATG CGG TAT GGG TGG TTG CCG CGG ACG TTG CAT Lys Met Val Leu Ala Met Arg Tyr Gly Trp Leu Pro Arg Thr Leu His 2935 2940 2945 2950	9665

	GTG GAT GAG CCG AGC CGG CAT GTG GAC TGG TCG GCT GGT GGT GTG CGG Val Asp Glu Pro Ser Arg His Val Asp Trp Ser Ala Gly Gly Val Arg 2955 2960 2965	9713
5	TTG CTG ACC GAG GCG CGG GAG TGG CCG GGG GTG GAC CGG CCG CGT CGG Leu Leu Thr Glu Ala Arg Glu Trp Pro Gly Val Asp Arg Pro Arg Arg 2970 2975 2980	9761
10	GCG GCG GTC TCC GCC TTC GGT GTC AGT GGT ACC AAC GCC CAT CTG ATC Ala Ala Val Ser Ala Phe Gly Val Ser Gly Thr Asn Ala His Leu Ile 2985 2990 2995	9809
15	CTC GAA GCC CCC GAA GCC CTC GAA GCC CTC GAA GCC ACC GAC GCC CCC Leu Glu Ala Pro Glu Ala Leu Glu Ala Leu Glu Ala Thr Asp Ala Pro 3000 3005 3010	9857
20	GAA GCC CCC GAA GCC CCC GAA GCC CCC GAC GTC ACC GAC GTC ACC GAA Glu Ala Pro Glu Ala Pro Asp Val Thr Asp Val Thr Glu 3015 3020 3025 3030	9905
25	GCC CTC GAA GCC CCC GAC GCC ACC GAG GCG GAG GGT GCG AAG GCT CCT Ala Leu Glu Ala Pro Asp Ala Thr Glu Ala Glu Gly Ala Lys Ala Pro 3035 3040 3045	9953
30	GGC AGT CCC GAA GAG GCA CAG CCT GCT GTG GGT GTG GTG CCG GTG GTG Gly Ser Pro Glu Glu Ala Gln Pro Ala Val Gly Val Val Pro Val Val 3050 3055 3060	10001
35	GTT TCG GGG CGT TCG CGG GTG GTG CGG GAG GCT GCG GGC CGG TTG Val Ser Gly Arg Ser Arg Val Val Val Arg Glu Ala Ala Gly Arg Leu 3065 3070 3075	10049
40	GGC GAG GTG GTG GAG GCC GGG GGT GTG GGG CTG GCG GAT GTG GCG GTG Ala Glu Val Val Glu Ala Gly Gly Val Gly Leu Ala Asp Val Ala Val 3080 3085 3090	10097
45	ACG ATG GCG GGC CGG TCG CGG TTT GGG TAT CGG GCG GTT GTG CTG GCT Thr Met Ala Gly Arg Ser Arg Phe Gly Tyr Arg Ala Val Val Leu Ala 3095 3100 3105 3110	10145
50	CGG CGT GAG GCT GAG CTT GCC GGG CGT TTG CGG GCG TTG GCG GGG GGT Arg Gly Glu Ala Glu Leu Ala Gly Arg Leu Arg Ala Leu Ala Gly Gly 3115 3120 3125	10193
55	GAT CCG GAC GCG GGT GTG GTC ACC GGT GCG GTG GTG GAC CCG GAG ACG Asp Pro Asp Ala Gly Val Val Thr Gly Ala Val Val Asp Pro Glu Thr 3130 3135 3140	10241
	GGG TCC GGT GGT GGG GGC GTG GTG TTG GTT TTC CCT GGT CAG GGG ACG Gly Ser Gly Gly Gly Val Val Leu Val Phe Pro Gly Gln Gly Thr 3145 3150 3155	10289
	CAG TGG GTG GGG ATG GGT GCG GGG CTG CTG GGG TCT TCG GAG GTC TTT Gln Trp Val Gly Met Gly Ala Gly Leu Leu Gly Ser Ser Glu Val Phe 3160 3165 3170	10337
	GCG GCG TCG ATG CGG GAG TGT GCG CGG GCG CTG AGT GTT CAT GTG GAG Ala Ala Ser Met Arg Glu Cys Ala Arg Ala Leu Ser Val His Val Glu 3175 3180 3185 3190	10385

	TGG GAT TTG CTG GAG GTG TCG GGC GGG GCC GGG TTG GAG CGG GTG Trp Asp Leu Leu Glu Val Val Ser Gly Gly Ala Gly Leu Glu Arg Val 3195 3200 3205	10433
5	GAT GTG GTG CAG CCC GTG ACG TGG GCG GTG ATG GTG TCG CTG GCC CGG Asp Val Val Gin Pro Val Thr Trp Ala Val Met Val Ser Leu Ala Arg 3210 3215 3220	10481
10	TAC TGG CAG GCG ATG GGT GTG GAC GTG CCT GCG GTG GTG GGT CAT TCC Tyr Trp Gln Ala Met Gly Val Asp Val Ala Ala Val Val Gly His Ser 3225 3230 3235	10529
15	CAG GGG GAG ATC GCT GCT GCC ACG GTG GCG GGG GCG TTG TCG CTG GAG Gln Gly Glu Ile Ala Ala Ala Thr Val Ala Gly Ala Leu Ser Leu Glu 3240 3245 3250	10577
20	GAT GCG GCG GCT GTG GTC GCT CTG CGG GCG GGG TTG ATT GCC CGG TAT Asp Ala Ala Ala Val Val Ala Leu Arg Ala Gly Leu Ile Gly Arg Tyr 3255 3260 3265 3270	10625
25	CTG GCG GGT CGT GGT GCG ATG GCG GCT GTT CCG CTG CCT GCC GGC GAG Leu Ala Gly Arg Gly Ala Met Ala Ala Val Pro Leu Pro Ala Gly Glu 3275 3280 3285	10673
30	GTC GAG GCC GGG CTG GCG AAG TGG CCC GGA GTA CAG GTA GCC GCG GTC Val Glu Ala Gly Leu Ala Lys Trp Pro Gly Val Gln Val Ala Ala Val 3290 3295 3300	10721
35	AAC GGT CCG GCG TCC ACG GTG GTT TCC GGG GAT CGG CGG GCG GTG GCC Asn Gly Pro Ala Ser Thr Val Val Ser Gly Asp Arg Arg Ala Val Ala 3305 3310 3315	10769
40	GGT TAT GTG GCC GTC TGT CAG GCG GAG GGT GTG CAG GCT CGG TTG ATA Gly Tyr Val Ala Val Cys Gln Ala Glu Gly Val Gln Ala Arg Leu Ile 3320 3325 3330	10817
45	CCG GTG GAC TAC GCC TCT CAC TCC CGC CAT GTG GAG GAC CTG AAG GGC Pro Val Asp Tyr Ala Ser His Ser Arg His Val Glu Asp Leu Lys Gly 3335 3340 3345 3350	10865
50	GAG TTG GAG CGG GTG CTG TCC GGT ATC ATC CGC CCC CGC AGT CCG CGG GTG Glu Leu Glu Arg Val Leu Ser Gly Ile Arg Pro Arg Ser Pro Arg Val 3355 3360 3365	10913
55	CCG GTG TGT TCC ACC GTC GCC GGA GAG CAG CCG GGC GAG CCG GTT TTC Pro Val Cys Ser Thr Val Ala Gly Glu Gln Pro Gly Glu Pro Val Phe 3370 3375 3380	10961
	GAT GCG GGG TAT TGG TTC CGT AAT CTG CGG AAC CGG GTT GAG TTC TCC Asp Ala Gly Tyr Trp Phe Arg Asn Leu Arg Asn Arg Val Glu Phe Ser 3385 3390 3395	11009
	GGC GTG GTC GGT GGT TTG TTG GAG CAG GGC CAC CGT CGG TTC ATC GAG Ala Val Val Gly Gly Leu Leu Glu Gln Gly His Arg Arg Phe Ile Glu 3400 3405 3410	11057
	GTC AGT GCC CAC CCG GTA CTC GTC CAT GCC ATT GAG CAG ACG GCC GAG Val Ser Ala His Pro Val Leu Val His Ala Ile Glu Gln Thr Ala Glu 3415 3420 3425 3430	11105

	GCC GCG GAC CGG AGT GTC CAT GCC ACC GGA ACC CTG CGC CGC CAG GAC Ala Ala Asp Arg Ser Val His Ala Thr Gly Thr Leu Arg Arg Gln Asp 3435 3440 3445	11153
5	GAC AGC CCG CAC CGC CTG CTG ACC TCC ACC GCC GAG GCC TGG GCC CAC Asp Ser Pro His Arg Leu Leu Thr Ser Thr Ala Glu Ala Trp Ala His 3450 3455 3460	11201
10	GCC GCC ACC CTC ACC TGG GAC CCC GCC CTG CCC CCA GGT CAC CTC ACC Gly Ala Thr Leu Thr Trp Asp Pro Ala Leu Pro Pro Gly His Leu Thr 3465 3470 3475	11249
15	ACC CTC CCC ACC TAC CCC TTC AAC CAC CAC CAC TAC TGG GCC GTG ACA Thr Leu Pro Thr Tyr Pro Phe Asn His His His Tyr Trp Ala Val Thr 3480 3485 3490	11297
	TCC CCC GCC GGA GTC GGC GAC GCG GCT GCG GGC CGG TTC GGT ATG ACC Ser Pro Ala Gly Val Gly Asp Ala Ala Gly Arg Phe Gly Met Thr 3495 3500 3505 3510	11345
20	TGG GAG GAC CAC CCC TTC CTC CGT GGC GGG TTA CCC CTG GCC GAC TCC Trp Glu Asp His Pro Phe Leu Arg Gly Leu Pro Leu Ala Asp Ser 3515 3520 3525	11393
25	GGT GAG CGG GTG TTC GCC GGG CGG CTG GCG GGC TCC GAG CAC GAC TGG Gly Glu Arg Val Phe Ala Gly Arg Leu Ala Gly Ser Glu His Asp Trp 3530 3535 3540	11441
30	CTG ACG GAC CAT GCC GTG TCC GGG GTG ACG TTG CTG CCG GGT ACG GCC Leu Thr Asp His Ala Val Ser Gly Val Thr Leu Leu Pro Gly Thr Ala 3545 3550 3555	11489
	TTC GTG GAG TTC GCG CTG CAC GCG GGA GCC GCC ACC GGC TGC GGG CGG Phe Val Glu Phe Ala Leu His Ala Gly Ala Ala Thr Gly Cys Gly Arg 3560 3565 3570	11537
35	CTG GAA GAG CTG AGC GTT GAG GCG CCG TTG GTC TTG CCC GCC GCC GGT Leu Glu Glu Leu Ser Val Glu Ala Pro Leu Val Leu Pro Ala Ala Gly 3575 3580 3585 3590	11585
40	GGT GTG CGG GTG CAG ATG AGG GTG TCG GCC GCC GAC GAG TCG GGA CGG Gly Val Arg Val Gln Met Arg Val Ser Ala Ala Asp Glu Ser Gly Arg 3595 3600 3605	11633
	CGG AGG GTC GCC ATC CAC TCG GCC CCG GAA GCC GCC GTC CAC TCG GCC Arg Arg Val Ala Ile His Ser Ala Pro Glu Ala Ala Val His Ser Ala 3610 3615 3620	11681
45	GCA GAA CGC GGC GAC TCG GCC GGT GTC TGG ACG CGG CAC GGC GAG GGC Ala Glu Gly Gly Asp Ser Ala Gly Val Trp Thr Arg His Gly Glu Gly 3625 3630 3635	11729
50	ACG CTC GTG CCG GAC CCG GAG CCC ACG CCT CCG GAC GCC GAC TGG GCG Thr Leu Val Pro Asp Pro Glu Pro Thr Pro Pro Asp Ala Asp Trp Ala 3640 3645 3650	11777
55	CGG GCC TGG CCG CCC GCC GGG GAA CGC GTC GAA CCG GCC GAG CTC TAC Arg Ala Trp Pro Pro Ala Gly Glu Arg Val Glu Pro Ala Glu Leu Tyr 3655 3660 3665 3670	11825

	GAA CGG TTC GGG GCC CTG GGC TAC GAG TAC GGT GAG GCG TTC GCG GGC Glu Arg Phe Gly Ala Leu Gly Tyr Glu Tyr Gly Glu Ala Phe Ala Gly 3675 3680 3685	11873
5	GTG CGC GCC GTA TGG CGG CAG CCG GAC GCG CTG CTC GCC GAG GTG CTC Val Arg Ala Val Trp Arg Gln Pro Asp Ala Leu Leu Ala Glu Val Leu 3690 3695 3700	11921
10	CTG CCC GAC CGG GCC TCG ACC GGT GCC GGC CGG TTC GGT GTG CAC CCC Leu Pro Asp Arg Ala Ser Thr Gly Ala Gly Arg Phe Gly Val His Pro 3705 3710 3715	11969
15	GCG CTG CTG GAC GCG GCG CTG CAG CCG TGG ATC GCC GGT GGT CTC CTC Ala Leu Leu Asp Ala Ala Leu Gln Pro Trp Ile Ala Gly Gly Leu Leu 3720 3725 3730	12017
20	GAA GTG CCG GAG GAC GCA GTG CTG CTG CCC TTC GCC TGG CAG GGA GTG Glu Val Pro Glu Asp Ala Val Leu Leu Pro Phe Ala Trp Gln Gly Val 3735 3740 3745 3750	12065
25	TCG CTC TAC GCG ACG GGT GCC GGT GCT CTG CGG GTG CGG CTG ACG AAG Ser Leu Tyr Ala Thr Gly Ala Gly Ala Leu Arg Val Arg Leu Thr Lys 3755 3760 3765	12113
30	GCG GGT GAC GGG GCG GTC TCG CTC CAG GCC GCA GAC ACG TCC GGC GCG Ala Gly Asp Gly Ala Val Ser Leu Gln Ala Ala Asp Thr Ser Gly Ala 3770 3775 3780	12161
35	GCC GTG CTC TCC TTG GGG GCC CTG GTG ATG CGT CCG CTG GCG CGC CGG Ala Val Leu Ser Leu Gly Ala Leu Val Met Arg Pro Leu Ala Arg Arg 3785 3790 3795	12209
40	AAG CTG GAC GTG CTG CTC GGC ACG GAC GCC GGC GAA CGG TCG CTG TAC Lys Leu Asp Val Leu Leu Gly Thr Asp Ala Gly Glu Arg Ser Leu Tyr 3800 3805 3810	12257
45	CGC GTC GAG TGG CAG CCG CGG CTC CTG CCC GCC GGC CCG CCG CGC TCC Arg Val Glu Trp Gln Pro Arg Leu Leu Pro Ala Gly Pro Pro Arg Ser 3815 3820 3825 3830	12305
50	TGG GCG GTG CTC GGC CCC GAC GCG GAC CGG CTC GCC GGG ACG CCG GGC Trp Ala Val Leu Gly Pro Asp Ala Asp Arg Leu Ala Gly Thr Pro Gly 3835 3840 3845	12353
55	CTG GGG GAT CAG CCG GAC GGT GGG CCC ACC GCG CTG TAC CCG GAG GTG Leu Gly Asp Gln Pro Asp Gly Gly Pro Thr Ala Leu Tyr Pro Glu Val 3850 3855 3860	12401
	CGG GCG CTG CGG AAG GCG CTG GCG GCG GGC GCG CCG CGG CCG GAA GCG Arg Ala Leu Arg Lys Ala Leu Ala Ala Gly Ala Pro Arg Pro Glu Ala 3865 3870 3875	12449
	GTC GTA CTG CCG GTG CTC TCC GGG GCC GGG GCC ACT CCG GAG TCG GTG Val Val Leu Pro Val Leu Ser Gly Ala Gly Ala Thr Pro Glu Ser Val 3880 3885 3890	12497
	CGG CAG ACA ACG GAG CGC TGT CTG ACC GCG CTC CAG GAC TGG CTG GAC Arg Gln Thr Thr Glu Arg Cys Leu Thr Ala Leu Gln Asp Trp Leu Asp 3895 3900 3905 3910	12545

	GCC GAG GAG TTG GTG GAC ACA CCG CTC ATA GTG CTC ACC AGG GGA GCC Ala Glu Glu Leu Val Asp Thr Pro Leu Ile Val Leu Thr Arg Gly Ala 3915 3920 3925	12593
5	GTC GCC GCC GTA CCG GGG GAG GAG ATC GGG GAC CTG GCG TGT GCG GGG Val Ala Ala Val Pro Gly Glu Glu Ile Gly Asp Leu Ala Cys Ala Gly 3930 3935 3940	12641
10	GTG TGG GGC CTG GTG AGG TCC GCG CGG TCC GAG CAC CCG GGC CGC TTC Val Trp Gly Leu Val Arg Ser Ala Arg Ser Glu His Pro Gly Arg Phe 3945 3950 3955	12689
15	GCC CTC GTC GAC ACC GAC GGG CAT CCG GAC GAC CGC ACC CGC CTG CCC Ala Leu Val Asp Thr Asp Gly His Pro Asp Asp Arg Thr Ala Leu Pro 3960 3965 3970	12737
20	CTC GCG CTG CGC GCG GTC CTC GAC CGC GCC CGC CAG CTC TCC CTG CGG Leu Ala Leu Arg Ala Val Leu Asp Gly Ala Gly Gln Leu Ser Leu Arg 3975 3980 3985	12785
25	GCC GGC ACC GCC CGG ACC CCG GTC CTC CTC CGG GCC GGG ACC CCG GAG Ala Gly Thr Ala Arg Thr Pro Val Leu Leu Arg Ala Gly Thr Pro Glu 3995 4000 4005	12833
30	GAG CAG CGG GGT CCG GCA TTC GAC CCG GCG GGC ACG GTC CTG GTG ACG Glu Gln Arg Gly Pro Ala Phe Asp Pro Ala Gly Thr Val Leu Val Thr 4010 4015 4020	12881
35	GGC GCG ACC GGC ACG CTC GGG CGG CTG CTG GCC CGG CAT CTG GCC GCC Gly Ala Thr Gly Thr Leu Gly Arg Leu Leu Ala Arg His Leu Ala Ala 4025 4030 4035	12929
40	GAG CAC GGT GTG CGC CAT CTG CTG CTG AGC CGC GGC GGC CGG GCT Glu His Gly Val Arg His Leu Leu Leu Ser Arg Gly Gly Arg Ala 4040 4045 4050	12977
45	GCC GAA GGC GCG GAC GAA CTC GCC GCG GAA CTG GCC GGG TTG GAA GCC Ala Glu Gly Ala Asp Glu Leu Ala Ala Glu Leu Ala Gly Leu Glu Ala 4055 4060 4065	13025
50	GAG CCG TGC TTC GCG GCC TGT GAC GCG GCG GAC CGC GAG GCC CTG GCA Glu Pro Cys Phe Ala Ala Cys Asp Ala Ala Asp Arg Glu Ala Leu Ala 4075 4080 4085	13073
55	CGG GTG CTG GCG GAG GTG CCG GCC GAC CGG CGG CTG ACC CGA GTG ATC Arg Val Leu Ala Glu Val Pro Ala Asp Arg Pro Leu Thr Gly Val Ile 4090 4095 4100	13121
	CAC GCG GCC GGG GTG CTC GAC GAC GGC ACA CTC GAC GCG CTG ACC CCG His Ala Ala Gly Val Leu Asp Asp Gly Thr Leu Asp Ala Leu Thr Pro 4105 4110 4115	13169
	GAA CGG ATC GGT ACC GTC ATG CGG CCG AAG GCG GAC GCG GCG CTG AAC Glu Arg Ile Gly Thr Val Met Arg Pro Lys Ala Asp Ala Ala Leu Asn 4120 4125 4130	13217
	CTG CAC GAA CTG ACC CGG ACC AGC CCG CTG TCG GTG TTC GCG GTC TTC Leu His Glu Leu Thr Arg Thr Ser Pro Leu Ser Val Phe Ala Val Phe 4135 4140 4145	13265

	TCG GGC GCT GCC GGC ATC CTG GGC CGC CCC GGA CAG GCC AAC TAC GCC Ser Gly Ala Ala Gly Ile Leu Gly Arg Pro Gly Gln Ala Asn Tyr Ala 4155 4160 4165	13313
5	GCC GCC AAC ACC TTC CTC GAC GCG CTC GCG CAG CAC CGC CGC GCC CAC Ala Ala Asn Thr Phe Leu Asp Ala Leu Ala Gln His Arg Arg Ala His 4170 4175 4180	13361
10	GCC CTC CCC GCC GTG TCG CTC GCC TGG GGG CTG TGG GGC GGG GCG ACC Gly Leu Pro Ala Val Ser Leu Ala Trp Gly Leu Trp Gly Gly Ala Thr 4185 4190 4195	13409
15	GCC ATG ACC GGC CAT CTG TCC GGC ACC GAT CTG CGC CGG ATG CGC AGG Gly Met Thr Gly His Leu Ser Gly Thr Asp Leu Arg Arg Met Arg Arg 4200 4205 4210	13457
20	TCC GGT ATC GCG CCG ATG ACC CAC GAC CAG GGG CTC GCC CTG TTC GAC Ser Gly Ile Ala Pro Met Thr His Asp Gln Gly Leu Ala Leu Phe Asp 4215 4220 4225 4230	13505
25	CGA GCG CTC GCC GCC TCG GCC GAG GAC CCG CTG CTC GTA CCG ATG CGG Arg Ala Leu Ala Ser Ala Glu Asp Pro Leu Leu Val Pro Met Arg 4235 4240 4245	13553
30	CTG GAC CTG GCC GCC CTC GTC CGG GAG CGG GCC GAG CAC GGG CCG GAC Leu Asp Leu Ala Ala Leu Val Arg Glu Arg Ala Glu His Gly Pro Asp 4250 4255 4260	13601
35	GCG GTG CCC GGA CCG CTG CTC GGG CTG CTG CCC GCC CGG GCC GCG GTG Ala Val Pro Gly Pro Leu Leu Gly Leu Leu Pro Ala Arg Ala Ala Val 4265 4270 4275	13649
40	CGG CAG GCG GCG GCA CCG GTA CGC GGC GGA GCC CCC GCC CCC GCC GGC Arg Gln Ala Ala Ala Pro Val Arg Gly Gly Ala Pro Ala Pro Ala Gly 4280 4285 4290	13697
45	GGC GAG GGG ACG GCC GAG CGG CTG GCC GGG CTC GGG GAG GAG GCC AGG Gly Glu Gly Thr Ala Glu Arg Leu Ala Gly Leu Gly Glu Ala Arg 4295 4300 4305 4310	13745
50	CTG CGC GAG CTG GTG AGG CTG GTC CGC GCC GAG GTG TCG GGC GTG CTG Leu Arg Glu Leu Val Arg Leu Val Arg Ala Glu Val Ser Gly Val Leu 4315 4320 4325	13793
55	GGC TAC TCG GGC CCG GAC GCG GTG GAG CCC GGG CGC CCG TTC AAG GAT Gly Tyr Ser Gly Pro Asp Ala Val Glu Pro Gly Arg Pro Phe Lys Asp 4330 4335 4340	13841
	CTC GGC TTC GAC TCG CTG ACC GCC GTG GAG CTG CGC AAC CGC CTC GGC Leu Gly Phe Asp Ser Leu Thr Ala Val Glu Leu Arg Asn Arg Leu Gly 4345 4350 4355	13889
	GCC GCC ACC GGG CTG CGG CTG CCG ACC GCG CTG GTC TTC GAC CGC CCG Ala Ala Thr Gly Leu Arg Leu Pro Thr Ala Leu Val Phe Asp Arg Pro 4360 4365 4370	13937
	ACG TCC CAG GCA GTG GCC GAG TAC CTC GCT GCC GAA CTG GCC GGA CCG Thr Ser Gln Ala Val Ala Glu Tyr Leu Ala Ala Glu Leu Ala Gly Pro 4375 4380 4385 4390	13985

	CGG GAC GGC GGC GAC ACC GCG GCC GCG TTC GAG GGC CTG GAG GCG Arg Asp Gly Gly Asp Thr Ala Ala Ala Ala Phe Glu Gly Leu Glu Ala 4395 4400 4405	14033
5	CTG GCC GCG GCG GTG GGC GCG CTG GCC GAG GAC GAT CTG CGG CGC GAC Leu Ala Ala Ala Val Gly Ala Leu Ala Glu Asp Asp Leu Arg Arg Asp 4410 4415 4420	14081
10	GTG CTC CGG CGG CGA CTG ACC GAA CTG GCC GCC GCG CTC ACC CCG CAG Val Leu Arg Arg Arg Leu Thr Glu Leu Ala Ala Leu Thr Pro Gln 4425 4430 4435	14129
15	GGC CGG AAC CCC TCC GCG CCC GCA CCC GCC CCG TCC GAT CTG GAC GAG Gly Arg Asn Pro Ser Ala Pro Ala Pro Ser Asp Leu Asp Glu 4440 4445 4450	14177
	CGG CTG GAC TCC GCG AAC GAC GAC GAC CTC TTC GCC TTC ATC GAG GAG Arg Leu Asp Ser Ala Asn Asp Asp Asp Leu Phe Ala Phe Ile Glu Glu 4455 4460 4465 4470	14225
20	CAG CTT TGA GCAGCGAGAA CGACAGCAGC GAGAACGACG GCGACGACAC Gln Leu *	14274
	GGCCGGGGCA GCTCCGGGGA CGGCTCCGGG GGCTCCCCC CGGCAGGACG ACCGGGTCAG	14334
25	GGAGTATCTG AAGCGG GTG ACC GCC GAA CTG GTC GCC ACC CGC AAG CGG Met Thr Ala Glu Leu Val Ala Thr Arg Lys Arg 1 5 10	14383
30	CTC GGC GCG CTG GAG GAG CGG GCC CGC GAA CCG ATC GCC GTC GTC GCG Leu Gly Ala Leu Glu Ala Arg Ala Arg Glu Pro Ile Ala Val Val Ala 15 20 25	14431
	ATG AGC TGC CGC TAC CCG GGC GGG GTG ACG ACC CCC GAG GAC CTG TGG Met Ser Cys Arg Tyr Pro Gly Gly Val Thr Thr Pro Glu Asp Leu Trp 30 35 40	14479
35	CGG CTT CTC GCG GAC GAA CGC GAC GCC GTA TCC GGA CTT CCC CGG GAC Arg Leu Ala Asp Glu Arg Asp Ala Val Ser Gly Leu Pro Arg Asp 45 50 55	14527
40	CGC GGC TGG GAC CTG GAC GCC CTC TAC GAC CCC GAC GGC GGC CCC GGC Arg Gly Trp Asp Leu Asp Ala Leu Tyr Asp Pro Asp Gly Gly Pro Gly 60 65 70 75	14575
45	ACC AGC TAC GCC CGC GAA GGC GGC TTC CTG AGC CAC TGC GCC GGA TTC Thr Ser Tyr Ala Arg Glu Gly Gly Phe Leu Ser His Cys Ala Gly Phe 80 85 90	14623
	GAC GCG GAG TTC TTC GGC ATC TCC CCG CGC GAG GCG CTG GCG ATG GAC Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp 95 100 105	14671
50	CCG CAG CAG CGG CTG CTG GAG ACC TCC TGG GAG GCC CTG GAA CGC Pro Gln Gln Arg Leu Leu Leu Glu Thr Ser Trp Glu Ala Leu Glu Arg 110 115 120	14719
55	GCC GGA GTC ACC GCC GAC CGC GCC CGG GGC AGC CGG ACG GGC GTG TAC Ala Gly Val Thr Ala Asp Arg Ala Arg Gly Ser Arg Thr Gly Val Tyr	14767

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	125	130	135	
5	GCG GGC GTC ATG TAC GAC GAC TAC GGC GCC CGG GTG CTG TAC GGC GCC Ala Gly Val Met Tyr Asp Asp Tyr Gly Ala Arg Val Leu Tyr Gly Ala 140 145 150 155			14815
	Gly Ala Gly Pro Pro Glu Asp Leu Glu Gly Tyr Leu Val Asn Gly Ser 160 165 170			14863
10	GCG GGC AGC ATC GCC TCC GGC CGT GTC TCC TAC ACG TTC GGG CTG CGC Ala Gly Ser Ile Ala Ser Gly Arg Val Ser Tyr Thr Phe Gly Leu Arg 175 180 185			14911
15	GGC CCC GCG GTC ACC GTC AAT ACG GCC TGT TCG TCG TCA CTG GTG TCG Gly Pro Ala Val Thr Val Asn Thr Ala Cys Ser Ser Leu Val Ser 190 195 200			14959
20	CTC CAT CTG GCG GTG CGT GCC CTG CGG AAC GGC GAG TGC GAC ATG GCA Leu His Leu Ala Val Arg Ala Leu Arg Asn Gly Glu Cys Asp Met Ala 205 210 215			15007
	CTG GCC GGG GCG ACG GTG CTG TCC ACC CCC ACC GTG CTC GTG GAC Leu Ala Gly Gly Ala Thr Val Leu Ser Thr Pro Thr Val Leu Val Asp 220 225 230 235			15055
25	TTC TCC CGC CAG CGC GGT CTG GCC CCC GAC GGC CGC TGC AAG GCG TTC Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg Cys Lys Ala Phe 240 245 250			15103
30	GCC GAC TCC GCC GAC GGC ACC TCC TGG GCC GAG GGC GCC GGA ATG CTG Ala Asp Ser Ala Asp Gly Thr Ser Trp Ala Glu Gly Ala Gly Met Leu 255 260 265			15151
35	CTG CTC CAG CGG CTG TCC GAC GCC CGC CGC GAG GGG CCC CCC GTG CTG Leu Leu Gln Arg Leu Ser Asp Ala Arg Arg Glu Gly Arg Pro Val Leu 270 275 280			15199
	GCC GTC ATT CGC GGC TCG GCC GTC AAC CAG GAC GGC GCC AGC AAC GGA Ala Val Ile Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly 285 290 295			15247
40	CTG ACC GCC CCC AAC GGG CGG GCG CAG CGG CAG GTC ATC GAG GAC GCG Leu Thr Ala Pro Asn Gly Arg Ala Gln Arg Gln Val Ile Glu Asp Ala 300 305 310 315			15295
45	CTG CGC GAC GCC GGG GTC GGC CCC GAC CAG GTC GAC GCG GTC GAG GCG Leu Arg Asp Ala Gly Val Gly Pro Asp Gln Val Asp Ala Val Glu Ala 320 325 330			15343
	CAT GGC ACC GGT ACC GAG CTG GGC GAC CCC ATC GAG GGC GGG GCG CTG His Gly Thr Gly Thr Glu Leu Gly Asp Pro Ile Glu Ala Gly Ala Leu 335 340 345			15391
50	CTC GCC ACC TAT GGA ACG GCC CGT ACG GCG GAG CGC CCG CTG TGG CTC Leu Ala Thr Tyr Gly Thr Ala Arg Thr Ala Glu Arg Pro Leu Trp Leu 350 355 360			15439
55	GGC TCC CTG AAG TCC AAC ATC GGG CAC ACC CAG GCC GCC GGC GGT GTT Gly Ser Leu Lys Ser Asn Ile Gly His Thr Gln Ala Ala Gly Val			15487

	365	370	375	
5	GCG GGC GTC ATC AAG ATG GTG CTG GCG ATG CCG CAC GGC CGG CTG CCC Ala Gly Val Ile Lys Met Val Leu Ala Met Arg His Gly Arg Leu Pro 380 385 390 395			15535
	CGC ACC CTG CAC GTG GAC CGG CCC ACC ACC CGG GTG GAC TGG GAG AAG Arg Thr Leu His Val Asp Arg Pro Thr Thr Arg Val Asp Trp Glu Lys 400 405 410			15583
10	GCG GGG GTG CGG CTC CTC ACG GAG CCG GTG CCA TGG CCG GGG GAA GCG Gly Gly Val Arg Leu Leu Thr Glu Pro Val Pro Trp Pro Gly Glu Ala 415 420 425			15631
15	GGG GAG CCG CGT CGC GCG GGC GTG TCC TCC TTC GGC GCG AGC GGC ACG Gly Glu Pro Arg Arg Ala Gly Val Ser Ser Phe Gly Ala Ser Gly Thr 430 435 440			15679
20	AAC GCG CAT GTG GTG CTG GAG AGC GTC CCG GCC GGT GAA CCG CCC GCC Asn Ala His Val Val Leu Glu Ser Val Pro Ala Gly Glu Pro Pro Ala 445 450 455			15727
	GCC GGG CGG CCG GAG GAC ACA GGC GGC GCC TGG ACG GTC AGC GGC CGC Ala Gly Arg Pro Glu Asp Thr Gly Gly Ala Trp Thr Val Ser Gly Arg 460 465 470 475			15775
25	GCC CCG GCG GCC CTG CGC GCC CAG GCC CGG CTG TAC GAC GCG CTC Gly Pro Ala Ala Leu Arg Ala Gln Ala Ala Arg Leu Tyr Asp Ala Leu 480 485 490			15823
30	ACC GGC ACC GGC ACC GGC ACC GGA CAG GGC GCC GGA CAG GGC CCC GGA Thr Gly Thr Gly Thr Gly Gln Gly Ala Gly Gln Gly Ala Gly 495 500 505			15871
	CCC GGC ACC GCC GAG GTG GCC GGC GCG CTG GCC CAC GCC CGT ACC GCG Pro Gly Thr Ala Glu Val Ala Gly Ala Leu Ala His Ala Arg Thr Ala 510 515 520			15919
35	TTC CGG CAC CGG GCC GTC GTG CTC GGC GGA AAC CGC GCC GAA CTG CTC Phe Arg His Arg Ala Val Val Leu Gly Gly Asn Arg Ala Glu Leu Leu 525 530 535			15967
40	GCG GGG CTG CGC GAG CTG GCG GAG GAG CAT CCC GGA CCC CGC GTG Ala Gly Leu Arg Glu Leu Ala Glu Glu His Pro Gly Pro Arg Val 540 545 550 555			16015
45	GTC ACA GGG ACC GCC CCG GCC ACC GAG CGG CGG ACG GCC TTC CTC TTC Val Thr Gly Thr Ala Pro Ala Thr Glu Arg Arg Thr Ala Phe Leu Phe 560 565 570			16063
	TCC GGG CAG GGC AGC CAG CGG GCC TCC GGC CGG GGC CTG TAC CGC Ser Gly Gln Gly Ser Gln Arg Ala Gly Ser Gly Arg Gly Leu Tyr Arg 575 580 585			16111
50	CGC CAC CCG GTC TTC GCC CGC GCC CTC GAC GAG GTG TGC GCC GCG CTC Arg His Pro Val Phe Ala Arg Ala Leu Asp Glu Val Cys Ala Ala Leu 590 595 600			16159
55	GAA CCG CAT CTT CAC CGC CCC CTG CGT GAC CTG ATG TTC GCC GAG CCC Glu Pro His Leu His Arg Pro Leu Arg Asp Leu Met Phe Ala Glu Pro			16207

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	605	610	615	
5	GGC AGC CCG GAA GCG GAG CCG CTC GAC CGC ACC GAG TTC ACC CAG CCC Gly Ser Pro Glu Ala Glu Pro Leu Asp Arg Thr Glu Phe Thr Gln Pro 620 625 630 635			16255
	GCG CTG TTC GCG CTC CAG ACC GCC CTG TTC CGG CTG GCC GAG CAC CAC Ala Leu Phe Ala Leu Gln Thr Ala Leu Phe Arg Leu Ala Glu His His 640 645 650			16303
10	GGC CTG CGC GCC GAG GCG CTG TGC GGG CAC AGC GTC GGC GAG ATC GCG Gly Leu Arg Ala Glu Ala Leu Cys Gly His Ser Val Gly Glu Ile Ala 655 660 665			16351
15	GCC GCC CAT GCC GCC GGT GTG CTG ACC CTG CCC GAC GCG GCC CGT CTG Ala Ala His Ala Ala Gly Val Leu Thr Leu Pro Asp Ala Ala Arg Leu 670 675 680			16399
20	GTG GCC CCC CGG GGA CGG CTG ATG CAG GCC CTG CCG GCC GGC GGT GCC Val Ala Ala Arg Gly Arg Leu Met Gln Ala Leu Pro Ala Gly Gly Ala 685 690 695			16447
	ATG GCC GCG CTG CGC GCC ACC GCC GAG GAG ATC GCA CCA CTG CTG GAG Met Ala Ala Leu Arg Ala Thr Ala Glu Glu Ile Ala Pro Leu Leu Glu .700 705 710 715			16495
25	CGC CGC GCG GGC GAA CTG GCG CTC GCC GTC AAC GGC CCC TCC TCG Arg Arg Ala Gly Glu Leu Ala Leu Ala Val Asn Gly Pro Ser Ser 720 725 730			16543
30	GTG GTG GTG TCG GGC GAC GAG GCC GCC GTC CTG GAG CTA CTG GAG CAG Val Val Val Ser Gly Asp Glu Ala Ala Val Leu Glu Leu Leu Glu Gln 735 740 745			16591
35	TGG CGG GCC GAG GGC CGC GAG GCC AGG CGG CTC GCC GTC AGC CAT GCC Trp Arg Ala Glu Gly Arg Glu Ala Arg Arg Leu Ala Val Ser His Ala 750 755 760			16639
	TTC CAT TCA CCG CGG ATG GAC GGA ATG TTG ACA CAG TTC GAC CGG GTC Phe His Ser Pro Arg Met Asp Gly Met Leu Thr Gln Phe Asp Arg Val 765 770 775			16687
40	GCT CGC ACC CTG ACG TTC GCT CCG CCG ACC ATT CCC CTC GTG TCC ACC Ala Arg Thr Leu Thr Phe Ala Pro Pro Thr Ile Pro Leu Val Ser Thr 780 785 790 795			16735
45	CTC ACC GGT ACG CCC GTC ACC GAG GAA ACC CTG TGC ACC GCG GAC CAC Leu Thr Gly Thr Pro Val Thr Glu Glu Thr Leu Cys Thr Ala Asp His 800 805 810			16783
	TGG GTC CGC CAG GCG CGC GAG CCG GTG CGC TTC CTG GAC GCC ATG CGG Trp Val Arg Gln Ala Arg Glu Pro Val Arg Phe Leu Asp Ala Met Arg 815 820 825			16831
50	ACC CTG CGC GCC GAC GGG ATC GAC ACC TTC GTG GAA CTC GCG CCC GAC Thr Leu Arg Ala Asp Gly Ile Asp Thr Phe Val Glu Leu Gly Pro Asp 830 835 840			16879
55	GGC GTG CTG TCC GCC ATG GCC CGC GAC TGC GCG GAC GAC CGG CCC GAT Gly Val Leu Ser Ala Met Ala Arg Asp Cys Ala Asp Asp Arg Pro Asp			16927

	845	850	855	
5	GCC GAC ACA ACC GGG GCC GGG GAC GGG GAG ACC CCC GAT CCG CTG CTC Gly Asp Thr Thr Gly Ala Gly Asp Gly Glu Thr Pro Asp Pro Leu Leu 860 865 870 875			16975
	ACC CTC CCG CTG CTG CGC CGC TCC GTG CCC GAG ACC GCC GAC GCC GAA Thr Leu Pro Leu Leu Arg Arg Ser Val Pro Glu Thr Gly Asp Ala Glu 880 885 890			17023
10	CAC CCC GGC GGC TTC GAA CGG GCC CTG GCC ACC GCC TAC GCA CAC GCC His Pro Gly Gly Phe Glu Arg Ala Leu Ala Thr Ala Tyr Ala His Gly 895 900 905			17071
15	GTC CCC CTG CGG CTC GCG CCC GCC CCC GAC GCC GCG TCC CTC GCC GTG Val Pro Leu Arg Leu Ala Pro Ala Pro Asp Ala Ala Ser Leu Ala Val 910 915 920			17119
20	GCC GCC GAA CTG CCC ACC TAC GCC TTC CAG CGC ACC CAC TAC TGG CTC Ala Ala Glu Leu Pro Thr Tyr Ala Phe Gln Arg Thr His Tyr Trp Leu 925 930 935			17167
	GAC GCG CCC GCC CCC GCC CTC CCC GCC GGG CTC GAC GAC GAC GCC Asp Ala Pro Ala Ala Pro Ala Ala Leu Pro Ala Gly Leu Asp Asp Ala 940 945 950 955			17215
25	GGT CAC CCG CTG CTC TCC GCG GCC CTC GAC CTG CCC GGC GGA CGC GGA Gly His Pro Leu Leu Ser Ala Ala Leu Asp Leu Pro Gly Gly Arg Gly 960 965 970			17263
30	ACG GTG TGG ACC GGA GCG CTC TCC GCG GCC ACC CTG CCC TGG GCC GCG Thr Val Trp Thr Gly Ala Leu Ser Ala Ala Thr Leu Pro Trp Ala Ala 975 980 985			17311
35	GAC CAC AGC GTG CAC GGC CGC ACC GTC CTG CCG GGC ACC GCC CTG CTC Asp His Ser Val His Gly Arg Thr Val Leu Pro Gly Thr Ala Leu Leu 990 995 1000			17359
	GAC CTG GCG CTC CAC GCC CCC CGC GTC GGC GAG TTG ACC TTC GAG Asp Leu Ala Leu His Ala Ala Pro Arg Val Gly Glu Leu Thr Phe Glu 1005 1010 1015			17407
40	GCG CCG CTG GTG CTG CCG GAG GAC GGA GAG GTC CGG CTG CGC GTC GTA Ala Pro Leu Val Leu Pro Glu Asp Gly Glu Val Arg Leu Arg Val Val 1020 1025 1030 1035			17455
45	CTC GCT GAA CCG GAC GCG AGC GGA GTA CGC GAA CTG TCT GTC CAC TCC Leu Ala Glu Pro Asp Ala Ser Gly Val Arg Glu Leu Ser Val His Ser 1040 1045 1050			17503
	GCC GGC GAG GAC GGC GGC TGG ACC CGG CAC GCG ACA GCG GTC CTG GAC Ala Gly Glu Asp Gly Gly Trp Thr Arg His Ala Thr Ala Val Leu Asp 1055 1060 1065			17551
50	ACC GGC ACC ACC ACC GCC GGG GAG CCC GCC GGC GCA CCG CCC GCC GCA Thr Gly Thr Thr Ala Gly Glu Pro Ala Gly Ala Pro Pro Ala Ala 1070 1075 1080			17599
55	TGG CCG CCC GGG GAC GCC GAA CCC CTC GAC CTT GCC GGC GAG TAC GAG Trp Pro Pro Gly Asp Ala Glu Pro Leu Asp Leu Ala Glu Tyr Glu			17647

	1085	1090	1095	
5	CGC TTC GCC GAC GCC GGC ATC GGA TAC GGC CCC GCC TTC CGC GGA CTG Arg Phe Ala Asp Ala Gly Ile Gly Tyr Gly Pro Ala Phe Arg Gly Leu 1100 1105 1110 1115			17695
	CGC TCC GCC TGG CGC GAC GGC GCG ATA CTG GCC GAC GTA CGG CTG Arg Ser Ala Trp Arg Asp Gly Asp Ala Ile Leu Ala Asp Val Arg Leu 1120 1125 1130			17743
10	CCC GGC GAA CTG GCC CGC GAA GCC GAC CGG TAC GGC ATC CAC CCG GCC Pro Gly Glu Leu Ala Gly Glu Ala Asp Arg Tyr Gly Ile His Pro Ala 1135 1140 1145			17791
15	CTG CTC GAC GCC GCC CTG CAC ACC GCG GCC GCG CTG GGA GGG GCG Leu Leu Asp Ala Ala Leu His Thr Ala Ala Ala Leu Gly Gly Ala 1150 1155 1160			17839
20	CAC GGG ATG CTG CCG TTC ACG TGG AAC GGC GTC ACC CTC CAC GCC CGC His Gly Met Leu Pro Phe Thr Trp Asn Gly Val Thr Leu His Ala Arg 1165 1170 1175			17887
	GGA GCG CAC GCC ATC CGG GTG CGG CTG ACC CCG GCC GGC CCC GAC GCG Gly Ala His Ala Ile Arg Val Arg Leu Thr Pro Ala Gly Pro Asp Ala 1180 1185 1190 1195			17935
25	GTC GCG GTC ACC GCC GTG GAC CCG GCG GGG CGC CCC GTG TTC ACG GCC Val Ala Val Thr Ala Val Asp Pro Ala Gly Arg Pro Val Phe Thr Ala 1200 1205 1210			17983
30	GCC TCG CTC ACC CTG CGA CCG GTC ACG ACC GGG CAG CTG ACC GCG GCC Ala Ser Leu Thr Leu Arg Pro Val Thr Thr Gly Gln Leu Thr Ala Ala 1215 1220 1225			18031
35	GAG GCC GCG CGG GCC CCG CTG TAC CGG GTG CGC TGG ACC GGC CTC CCG Glu Ala Ala Arg Ala Pro Leu Tyr Arg Val Arg Trp Thr Gly Leu Pro 1230 1235 1240			18079
	GAC ACC GGA ACC GCC CGG GAC CAC ACC TGG GCG GTG GCC GGC GGC CCG Asp Thr Gly Thr Ala Arg Asp His Thr Trp Ala Val Ala Gly Gly Pro 1245 1250 1255			18127
40	GGC GAC CTG TTA CCC CGG GAG ACC CCG CAC CAC CCC GAC CTC GCC TCC Gly Asp Leu Leu Pro Gly Glu Thr Pro His His Pro Asp Leu Ala Ser 1260 1265 1270 1275			18175
45	GCG CTC GCC GAC ACC GGC ACC GCC CCC TTC CGC GTA CTG GCG GAT CTG Ala Leu Ala Asp Thr Gly Thr Ala Pro Phe Arg Val Leu Ala Asp Leu 1280 1285 1290			18223
	CGC GGA TAC GGC ACC GCC ACC CCC CGG GAA CTC GCC TCC CAG GCG CTC Arg Gly Tyr Gly Thr Ala Thr Pro Arg Glu Leu Ala Ser Gln Ala Leu 1295 1300 1305			18271
50	GCC CTC GTC CAG CAG TGG GCC GAC GCG GCC GAG GCC GCC GAA GGC AGG Ala Leu Val Gln Gln Trp Ala Asp Ala Ala Glu Ala Ala Glu Gly Arg 1310 1315 1320			18319
55	CTC GTC CTG GTG ACA CGC CGG GCC GTC GAC ATC GGT GAC GGC GTC ACG Leu Val Leu Val Thr Arg Arg Ala Val Asp Ile Gly Asp Gly Val Thr			18367

	1325	1330	1335	
5	GAC CCG GCG GCG GCG ACC GTG TGG GGA CTG GTC CGG GCG GCA CAG TCC Asp Pro Ala Ala Ala Thr Val Trp Gly Leu Val Arg Ala Ala Gln Ser 1340 1345 1350 1355			18415
	GAG CAC CCC GGG TGC TTC GCG CTC CTC GAC ACC GAC GAC TCC CCC CGC Glu His Pro Gly Cys Phe Ala Leu Leu Asp Thr Asp Asp Ser Pro Arg 1360 1365 1370			18463
10	TCC CGG CAA CTC CTG CCA CGC GTC GCG GGC ACC GCC GAG CAG CTC GCA Ser Arg Gln Leu Leu Pro Arg Val Ala Gly Thr Ala Glu Gln Leu Ala 1375 1380 1385			18511
15	CTC CGC GAC GGC ACC CTG CTC GCC CCC TCC CTC ACC CGT GCC ACG CTG Leu Arg Asp Gly Thr Leu Leu Ala Pro Ser Leu Thr Arg Ala Thr Leu 1390 1395 1400			18559
20	CCC GCC GGC GCC CGG CTG CCC GCA CTC GAC GGC ACC GTC CTG ATC ACT Pro Ala Gly Ala Arg Leu Pro Ala Leu Asp Gly Thr Val Leu Ile Thr 1405 1410 1415			18607
	GGG GGC ACC GGC AGC CTC GGC GCG GAG GCG GCG CAT CTG GTC ACC Gly Gly Thr Gly Ser Leu Gly Ala Glu Ala Ala Arg His Leu Val Thr 1420 1425 1430 1435			18655
25	CGG CAC GGT GCC CGG CGC CTG CTC CTG ACC AGC CGA AGC GGC CCG CAG Arg His Gly Ala Arg Arg Leu Leu Leu Thr Ser Arg Ser Gly Pro Gln 1440 1445 1450			18703
30	GCC CCC GGC GCG GCC GAA CTC GTC GCC GAA CTG GCC GCC TTG GGC GCC Ala Pro Gly Ala Ala Glu Leu Val Ala Glu Leu Ala Ala Leu Gly Ala 1455 1460 1465			18751
	CAC GCG GAC GTG GCC GCC TGC GAC GTC GCC GAC CGC GCC GCC CTG CGG His Ala Asp Val Ala Ala Cys Asp Val Ala Asp Arg Ala Ala Leu Arg 1470 1475 1480			18799
35	GCC CTG CTC GAC CGC GTA CCC GCC GGC CAC CCG CTG ACC GCG GTC CTG Ala Leu Leu Asp Arg Val Pro Ala Gly His Pro Leu Thr Ala Val Leu 1485 1490 1495			18847
40	CAC ACG GCG GGC GTC CTG GAC GAC GGC GTC CTC ACC GCC CAG ACA CGG His Thr Ala Gly Val Leu Asp Asp Gly Val Leu Thr Ala Gln Thr Pro 1500 1505 1510 1515			18895
45	CAG CGG CTC GCG GCC GTC CTC CGC CCG AAG GCC GAC GCC GTA CGC AAT Gln Arg Leu Ala Ala Val Leu Arg Pro Lys Ala Asp Ala Val Arg Asn 1520 1525 1530			18943
	CTG CAC GAA CTC ACC CAG GGG CAC GCC CTG TCG GCG TTC ATC CTC TAC Leu His Glu Leu Thr Gln Gly His Ala Leu Ser Ala Phe Ile Leu Tyr 1535 1540 1545			18991
50	TCG TCG GCC GCC GGA GTG CTC GGC AGC GCG GGC CAG AGC GGC TAC GCC Ser Ser Ala Ala Gly Val Leu Gly Ser Ala Gly Gln Ser Gly Tyr Ala 1550 1555 1560			19039
55	GCC GCC AAC GCC TAC CTG GAC TCC TTC GCC GTC TGG CGG CGG AGC CGG Ala Ala Asn Ala Tyr Leu Asp Ser Phe Ala Val Trp Arg Arg Ser Arg			19087

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	1565	1570	1575	
5	GGA CTG CCC GCC GTA TCG CTC GGC TGG GGC CCG TGG GAC GGC GGC GGC Gly Leu Pro Ala Val Ser Leu Gly Trp Gly Pro Trp Asp Gly Gly Gly 1580 1585 1590 1595			19135
	ATG GCG AGC GGA CTC GGC GGA ACC GAC ACG GCC CGG CTG CGG CGC AGC Met Ala Ser Gly Leu Gly Gly Thr Asp Thr Ala Arg Leu Arg Arg Ser 1600 1605 1610			19183
10	GCG ATC GCA CCC CTC AGC CGC GCC GAG GGC CTG GCC GCG CTC GAC GCG Gly Ile Ala Pro Leu Ser Arg Ala Glu Gly Leu Ala Ala Leu Asp Ala 1615 1620 1625			19231
15	GCG CTC GCG GCC GGC GGC GAC GAC ACC GCG CCG GCC CAC CTG CTG CCG Ala Leu Ala Ala Gly Gly Asp Asp Thr Ala Pro Ala His Leu Leu Pro 1630 1635 1640			19279
20	ATC CGC GTC GAC GCG GTG ACC CTG CGC GGC GCC GAC ACC GTC CCC GCC Ile Arg Val Asp Ala Val Thr Leu Arg Gly Ala Asp Thr Val Pro Ala 1645 1650 1655			19327
	GTG CTG CGC GAC CTG GCG GGA ACC GCG CCA AGC GCC GCC GAA CGG CCC Val Leu Arg Asp Leu Ala Gly Thr Ala Pro Ser Ala Ala Glu Arg Pro 1660 1665 1670 1675			19375
25	CCC GGG ACA CCG GAG GAC ACG AAC GCG CCC CTG CGC GAC GTC ACC CAA Pro Gly Thr Pro Glu Asp Thr Asn Ala Pro Leu Ala Asp Val Thr Gln 1680 1685 1690			19423
30	CTG CAC CGC CGG GAA CGG AAG GAG GCA CTG ACC GGC TTC GTC CCC GCC Leu His Gly Arg Glu Arg Lys Glu Ala Leu Thr Gly Phe Val Arg Ala 1695 1700 1705			19471
35	CAG GTG GCC GCG GTG CTC GGC CAC CCC ACG TCC GAC ACG ATC GAC GTC Gln Val Ala Ala Val Leu Gly His Pro Thr Ser Asp Thr Ile Asp Val 1710 1715 1720			19519
	CGC CGG AGC TTC AAG GAA GCG GGC TTC GAC TCC CTC ACC GCC GTC GAA Arg Arg Ser Phe Lys Glu Ala Gly Phe Asp Ser Leu Thr Ala Val Glu 1725 1730 1735			19567
40	CTG CGC AAC CGG CTG CGC GCC ACC GGG CTG AAG CTG CCC GCC ACG Leu Arg Asn Arg Leu Arg Ala Ala Thr Gly Leu Lys Leu Pro Ala Thr 1740 1745 1750 1755			19615
45	CTG GTG TTC GAC CAC CCG ACC CCC CTC GCG CTC GCC GGC TTC CTC CAC Leu Val Phe Asp His Pro Thr Pro Leu Ala Leu Ala Gly Phe Leu His 1760 1765 1770			19663
	CGC GAA CTC CCC GGC GCC GAA GCC TCC CTG ATG AGC GCG ATC GAC ACT Arg Glu Leu Pro Gly Ala Glu Ala Ser Leu Met Ser Ala Ile Asp Thr 1775 1780 1785			19711
50	CTC CGG CAC CGG CTG CGC GAC GCC CTG GCC GAC GAC GCC GCA GAC GAC Leu Arg His Arg Leu Arg Asp Ala Leu Ala Asp Asp Ala Ala Asp Asp 1790 1795 1800			19759
55	GCC CTG CGC GAC CAG ATC ACC CGA CGA CTC GAG ACC CTG CTG GCC GGC Ala Leu Arg Asp Gln Ile Thr Arg Arg Leu Glu Thr Leu Leu Ala Gly			19807

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	1805	1810	1815	
5	ATA GCC CGG ACC GAG GAG CCC GCG CCC GCC ACC GCC GCC GAC GAC Ile Ala Arg Thr Glu Glu Pro Ala Pro Ala Thr Ala Ala Ala Asp Asp 1820 1825 1830 1835			19855
	GGG AGC GGA GCC GGT GAT GTC GCG GAA CGA CTG AGC ACC GCG TCG GAC Gly Ser Gly Ala Gly Asp Val Ala Glu Arg Leu Ser Thr Ala Ser Asp 1840 1845 1850			19903
10	GAC GAA CTG TTC GAA CTG CTC GAC AGC GGT TTC ACA CCC TGA CCGGCCGGCG Asp Glu Leu Phe Glu Leu Leu Asp Ser Gly Phe Thr Pro *1855 1860 1865			19955
15	GACGGCACCC ACGACATCGA GGCGACCGCA CCGAACACCCC CCAGGGGAA AGCT			20009
	GTG TCC ACC GAG AAC TCC ACC AAC GTC CCG GCG AGC GAG Met Ser Thr Glu Asn Ser Thr Asn Val Pro Ala Ser Glu 1 5 10			20048
20	GAC AAG CTC CGC GCC TAT CTG CGT CGC GCG ATG GCC GAC CTC CAC GAG Asp Lys Leu Arg Ala Tyr Leu Arg Arg Ala Met Ala Asp Leu His Glu 15 20 25			20096
25	TCC CGC GAA CGG CTC CGC GCC ACG GAA GCG CGC GCC CAG GAG CCG ATC Ser Arg Glu Arg Leu Arg Ala Thr Glu Ala Arg Ala Gln Glu Pro Ile 30 35 40 45			20144
	GGC GTG GTG GGT ATG GGG TGC CGG TTC CCC GGT GGG GTG GGT TCG CCG Ala Val Val Gly Met Gly Cys Arg Phe Pro Gly Gly Val Gly Ser Pro 50 55 60			20192
30	GAG GCG TTG TGG CGG TTG GTG GTG GAG GGG GTG GAC GCG GTT TCC CCG Glu Ala Leu Trp Arg Leu Val Val Glu Gly Val Asp Ala Val Ser Pro 65 70 75			20240
35	TTT CCC GGT GAT CGT GGC TGG GAT GTG GAG GGG TTG TAC GAC CCG GAG Phe Pro Gly Asp Arg Gly Trp Asp Val Glu Gly Leu Tyr Asp Pro Glu 80 85 90			20288
40	CCG GGT GTG GCG GGG AAG TCG TAT GTG CCG GAG GGG GGT TTT CTG CAT Pro Gly Val Ala Gly Lys Ser Tyr Val Arg Glu Gly Gly Phe Leu His 95 100 105			20336
	GAT GCG GCG GAG TTC GAT GCG GAG TTC TTC GGG ATT TCG CCG CGT GAG Asp Ala Ala Glu Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg Glu 110 115 120 125			20384
45	GCG GTG GCG ATG GAT CCG CAG CAG CGG CTG TTG CTG GAG ACC TCC TGG Ala Val Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr Ser Trp 130 135 140			20432
50	GAG GCG ATC GAG CGG GCG GGT ATC GAC CCG CAT TCG CTG CAC GGC AGC Glu Ala Ile Glu Arg Ala Gly Ile Asp Pro His Ser Leu His Gly Ser 145 150 155			20480
55	CGC ACC GGC GTC TAC GCC GGC GTG ATG TAC CAC GAC TAT GGC ACG GGA Arg Thr Gly Val Tyr Ala Gly Val Met Tyr His Asp Tyr Gly Thr Gly 160 165 170			20528

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	CAG ACC TCC GCG ACC GAC ACG AGC GGT TAT TCC GGC ACC GGT ACG TCG Gln Thr Ser Ala Thr Asp Thr Ser Gly Tyr Ser Gly Thr Gly Thr Ser 175 180 185	20576
5	GGG AGT GTG GTG TCG GGG CGT GTG GCC TAC ACG CTG GGG CTG GAG GGT Gly Ser Val Val Ser Gly Arg Val Ala Tyr Thr Leu Gly Leu Glu Gly 190 195 200 205	20624
10	CCG GCC GTG ACC GTG GAT ACG GCG TGT TCG TCG TTG GTG GCG TTG Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu 210 215 220	20672
15	CAT CTG GCG GTG CAG GCG TTG CCG GGT GGC GAG TGT GAC ATG GCG TTG His Leu Ala Val Gln Ala Leu Arg Gly Gly Glu Cys Asp Met Ala Leu 225 230 235	20720
20	GCC GGT GGT GTG ACG GTG ATG GCC GGG CCG GGG ATG TTC GTG GAG TTT Ala Gly Gly Val Thr Val Met Ala Gly Pro Gly Met Phe Val Glu Phe 240 245 250	20768
25	TCG CGG CAG CGG GGG TTG GCG GCC GAT GGG CCG TGC AAG GCG TTC GCG Ser Arg Gln Arg Gly Leu Ala Ala Asp Gly Arg Cys Lys Ala Phe Ala 255 260 265	20816
30	GAT GGG GCG GAT GGG ACC GCT TGG GCC GAG GGT GCG GGG GTG GTG CTG Asp Gly Ala Asp Gly Thr Ala Trp Ala Glu Gly Ala Gly Val Val Leu 270 275 280 285	20864
35	GTG GAG CGG TTG TCG GAT GCC CGG CGG TTG GGG CAT CCG GTG TTG GCG Val Glu Arg Leu Ser Asp Ala Arg Arg Leu Gly His Pro Val Leu Ala 290 295 300	20912
40	GTC GTG TGT CGG TCG GCG GTG AAT CAG GAC GGT GCG TCG AAT GGT TTG Val Val Cys Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu 305 310 315	20960
45	ACG GCG CCG AGT GGT CCG TCG CAG GAG CGG GTG ATT CGT CAG GCG TTG Thr Ala Pro Ser Gly Pro Ser Gln Glu Arg Val Ile Arg Gln Ala Leu 320 325 330	21008
50	GCG AAT GCG CGG TTG ACG GTG GCG GAT GTG GAT GTG GTG GAG GCG CAT Ala Asn Ala Arg Leu Thr Val Ala Asp Val Asp Val Val Glu Ala His 335 340 345	21056
55	GGG ACG GGG ACG CGG CTG GGT GAT CCG ATC GAG GCG CAG GCG TTG CTG Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Leu 350 355 360 365	21104
	GGG ACG TAT GGG CGG GAT CGT GAT GGT GGG CGT CCG GTG TGG TTG GGG Gly Thr Tyr Gly Arg Asp Arg Gly Gly Arg Pro Val Trp Leu Gly 370 375 380	21152
	TCG TTG AAG TCG AAT ATT GGT CAT GCT CAG GCG GCT GCG GGG GTG GCT Ser Leu Lys Ser Asn Ile Gly His Ala Gln Ala Ala Gly Val Ala 385 390 395	21200
	GGT GTG ATC AAG ATG GTG TTG GCG ATG CGG TAT GGG TGG TTG CCG CGG Gly Val Ile Lys Met Val Leu Ala Met Arg Tyr Gly Trp Leu Pro Arg 400 405 410	21248

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	ACG TTG CAT GTG GAT GAG CCG AGC CGG CAT GTG GAC TGG TCG GCT GGT Thr Leu His Val Asp Glu Pro Ser Arg His Val Asp Trp Ser Ala Gly 415 420 425	21296
5	GGT GTG TGG TTG CTG ACC GAG GCG CGG GAG TGG CCG GGG GTG GAC CGG Gly Val Trp Leu Leu Thr Glu Ala Arg Glu Trp Pro Gly Val Asp Arg 430 435 440 445	21344
10	CCG CGT CGG GCG GCG GTC TCC GCC TTT GGT GTC AGT GGT ACC AAC GCC Pro Arg Arg Ala Ala Val Ser Ala Phe Gly Val Ser Gly Thr Asn Ala 450 455 460	21392
15	CAT CTG ATC CTC GAA GCC CCC GAC ACC GCC GAG GCG GAG AGC GCC ACG His Leu Ile Leu Glu Ala Pro Asp Thr Ala Glu Ala Glu Ser Ala Thr 465 470 475	21440
20	ACC CCG GTC CGC TCT GAG GTG TCG GAG TCT GCT GCG GTC TTC GAT GCC Thr Pro Val Arg Ser Glu Val Ser Glu Ser Ala Ala Val Phe Asp Ala 480 485 490	21488
25	CGC AGT GGT GTG GTG CCG GTG GTT TCG GGG CGT TCG CGG GTG GTG Arg Ser Gly Val Val Pro Val Val Ser Gly Arg Ser Arg Val Val 495 500 505	21536
30	GTC CGG GAG GCT GCG GGC CGG TTG GCG GAG GTG GTG GAG GCC GGT GGT Val Arg Glu Ala Ala Gly Arg Leu Ala Glu Val Val Glu Ala Gly Gly 510 515 520 525	21584
35	GTG GGG CTG GCG GAT GTG GCG GTG ACG ATG GCG GGC CGG TCG CGG TTT Val Gly Leu Ala Asp Val Ala Val Thr Met Ala Gly Arg Ser Arg Phe 530 535 540	21632
40	GGG TAT CGG GCG GTT GTG CTG GCT CGG GGT GAG GCT GAG CTT GCC GGG Gly Tyr Arg Ala Val Val Leu Ala Arg Gly Glu Ala Glu Leu Ala Gly 545 550 555	21680
45	CGT TTG CGG GCG TTG GCG GGG GGT GAT CCG GAC GCG GGT GTG GTC ACG Arg Leu Arg Ala Leu Ala Gly Gly Asp Pro Asp Ala Gly Val Val Thr 560 565 570	21728
50	GGT GCG GTG GTG GAC CCG GAG ACG GGG TCC GGT GGT GGG GGG GTG CTG Gly Ala Val Val Asp Pro Glu Thr Gly Ser Gly Gly Gly Val Val 575 580 585	21776
55	TTG GTT TTC CCT GGT CAG GGG ACG CAG TGG GTG GGG ATG GGT GCG GGG Leu Val Phe Pro Gly Gln Gly Thr Gln Trp Val Gly Met Gly Ala Gly 590 595 600 605	21824
	CTG CTG GGG TCT TCG GAG GTG TTT GCG GCG TCG ATG CGG GAG TGT GCG Leu Leu Gly Ser Ser Glu Val Phe Ala Ala Ser Met Arg Glu Cys Ala 610 615 620	21872
	CGG GCG CTG AGT GTT CAT GTG GGG TGG GAT TTG CTG GAG GTG GTG TCG Arg Ala Leu Ser Val His Val Gly Trp Asp Leu Leu Glu Val Val Ser 625 630 635	21920
	GGC GGG GCC GGG TTG GAG CGG GTG GAT GTG GTG CAG CCG GTG ACG TGG Gly Gly Ala Gly Leu Glu Arg Val Asp Val Val Gln Pro Val Thr Trp 640 645 650	21968

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	GGC CTG ATG GTG TCG CTG GCC CGG TAC TGG CAG GCG ATG GGT GTG GAC Ala Val Met Val Ser Leu Ala Arg Tyr Trp Gln Ala Met Gly Val Asp 655 660 665	22016
5	GTG GCT GCG GTG GTG GGT CAT TCC CAG GGG GAG ATC GCT GCT GCC ACG Val Ala Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala Thr 670 675 680 685	22064
10	GTG GCG GGG GCG TTG TCG CTG GAG GAT GCG GCG GCT GTG GTC GCT CTG Val Ala Gly Ala Leu Ser Leu Glu Asp Ala Ala Ala Val Val Ala Leu 690 695 700	22112
15	CGG GCG GGG TTG ATT GGC CGG TAT CTG GCG GGT CGT GGT GCG ATG GCG Arg Ala Gly Leu Ile Gly Arg Tyr Leu Ala Gly Arg Gly Ala Met Ala 705 710 715	22160
20	GCT GTT CCG CTG CCT GCC GGC GAG GTC GAG GCC GGG CTG GCG AAG TGG Ala Val Pro Leu Pro Ala Gly Glu Val Glu Ala Gly Leu Ala Lys Trp 720 725 730	22208
25	CCG GGT GTG GAG GTC GCG GCG GTC AAC GGT CCG GCG TCT ACG GTG GTT Pro Gly Val Glu Val Ala Ala Val Asn Gly Pro Ala Ser Thr Val Val 735 740 745	22256
30	TCC GGG GAT CGG CGG GCG GTG GCC GGT TAT GTG GCC GTC TGT CAG GCG Ser Gly Asp Arg Arg Ala Val Ala Gly Tyr Val Ala Val Cys Gln Ala 750 755 760 765	22304
35	GAG GGT GTG CAG GCT CGG TTG ATA CCG GTG GAC TAC GCC TCT CAC TCC Glu Gly Val Gln Ala Arg Leu Ile Pro Val Asp Tyr Ala Ser His Ser 770 775 780	22352
40	CGC CAT GTG GAG GAC CTG AAG GGC GAG TTG GAG CGG GTG CTG TCC GGT Arg His Val Glu Asp Leu Lys Gly Glu Leu Glu Arg Val Leu Ser Gly 785 790 795	22400
45	ATC CGC CCG CGC AGT CCG CGG GTG CCG GTG TGT TCC ACC GTC GCC GGA Ile Arg Pro Arg Ser Pro Arg Val Pro Val Cys Ser Thr Val Ala Gly 800 805 810	22448
50	GAG CAG CCG GGC GAG CCG GTT TTC GAT GCG GGG TAT TGG TTC CGT AAT Glu Gln Pro Gly Glu Pro Val Phe Asp Ala Gly Tyr Trp Phe Arg Asn 815 820 825	22496
55	CTG CGG AAC CGG GTT GAG TTC TCC GCG GTG GTC GGT GGT TTG TTG GAG Leu Arg Asn Arg Val Glu Phe Ser Ala Val Val Gly Gly Leu Leu Glu 830 835 840 845	22544
	GAG GGC CAC CGT CGG TTC ATC GAG GTC AGT GCC CAC CCG GTA CTC GTT Glu Gly His Arg Arg Phe Ile Glu Val Ser Ala His Pro Val Leu Val 850 855 860	22592
	CAT GCC ATT GAG CAG ACG GCC GAG GCC GCG GAC CGG AGT GTC CAT GCC His Ala Ile Glu Gln Thr Ala Glu Ala Ala Asp Arg Ser Val His Ala 865 870 875	22640
	ACC GGG ACC CTG CGC CGC CAG GAC GAC AGC CCG CAC CGC CTG CTG ACC Thr Gly Thr Leu Arg Arg Gln Asp Asp Ser Pro His Arg Leu Leu Thr 880 885 890	22688

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	TCC ACC GCC GAG GCC TGG CCC CAC GGC GCC ACC CTC ACC TGG GAC CCC Ser Thr Ala Glu Ala Trp Ala His Gly Ala Thr Leu Thr Trp Asp Pro 895 900 905	22736
5	GCC CTG CCC CCA GGC CAC CTC ACC ACC CTC CCC ACC TAC CCC TTC AAC Ala Leu Pro Pro Gly His Leu Thr Thr Leu Pro Thr Tyr Pro Phe Asn 910 915 920 925	22784
10	CAC CAC CAC TAC TGG CTC GAC ACC ACC CCC ACC ACC CCC GCG ACG ACC His His His Tyr Trp Leu Asp Thr Thr Pro Thr Thr Pro Ala Thr Thr 930 935 940	22832
15	ACC CAG AGC CCC ACC GAT GCC CAG AAC CCC GCC GAC GCC CTT CCC TAC Thr Gln Ser Pro Thr Asp Ala Gln Asn Pro Ala Asp Ala Leu Pro Tyr 945 950 955	22880
20	AAG GTG AGT TGG AAG CGG TTG CGG GAC CAG GAC AGC TTG ACC GCG CGC Lys Val Ser Trp Lys Arg Leu Arg Asp Gln Asp Ser Leu Thr Ala Arg 960 965 970	22928
25	CTC GAC GGC CGA TGG CTG CTG GTG GTA CCG GAG GCG TCG GCG GAC CCG Leu Asp Gly Arg Trp Leu Leu Val Val Pro Glu Ala Ser Ala Asp Pro 975 980 985	22976
30	TCG GTT GCT GAG GGC GTC GCG CGC GAG CTG ACC GCG CGG GGC GCG ACC Ser Val Ala Glu Gly Val Ala Arg Glu Leu Thr Ala Arg Gly Ala Thr 990 995 1000 1005	23024
35	G TG GAG TCG CTG ACG GTC GAG CCG GGC GCC GAC CGT TCG CGG CTG CGC Val Glu Ser Leu Thr Val Glu Pro Gly Ala Asp Arg Ser Arg Leu Arg 1010 1015 1020	23072
40	GGG CTG CTG GTC GAC GCC ACG GAA CGG GAC GAA GCC GGG CCG CTG CGC Gly Leu Leu Val Asp Ala Thr Glu Arg Asp Glu Ala Gly Pro Leu Arg 1025 1030 1035	23120
45	GGG ATC GTC TCG CTG CTC GCG TTG GCC GGG GAC CAC GCC GGG GCC GAC Gly Ile Val Ser Leu Leu Ala Leu Ala Gly Asp His Ala Gly Ala Asp 1040 1045 1050	23168
50	GGG GCA CGC CCG GTG GTT CCG GCC GGC CTG GCA GCG TCA CTG GCG CTG Gly Ala Arg Pro Val Val Pro Ala Gly Leu Ala Ala Ser Leu Ala Leu 1055 1060 1065	23216
55	ATC CAG GCC GCG GGC GAC GCG GGC ACG GAG GCC GGG CTG TGG GCG GTG Ile Gln Ala Ala Gly Asp Ala Gly Thr Glu Ala Gly Leu Trp Ala Val 1070 1075 1080 1085	23264
	ACC CGC GGC GCC GTC GCG GCC GTG CCC GGT GAC GTA CCG GCG CCG TCG Thr Arg Gly Ala Val Ala Ala Val Pro Gly Asp Val Pro Ala Pro Ser 1090 1095 1100	23312
	CAG GCG CTG CTC TGG GGA TTC GGC CGG GTG GCC GGG ATC GAG CTG CCG Gln Ala Leu Leu Trp Gly Phe Gly Arg Val Ala Gly Ile Glu Leu Pro 1105 1110 1115	23360
	CAC TGC TGG GGC GGC CTG CTC GAC CTG CCG ACC GGG CCC GGC GAC TCC His Cys Trp Gly Gly Leu Leu Asp Leu Pro Thr Gly Pro Gly Asp Ser 1120 1125 1130	23408

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	GGG TTC CCG CAA CTG GCC GCG ACC CTG GCG GGC CGT CCC GCG GAG GAC Gly Phe Arg Gln Leu Ala Ala Thr Leu Ala Gly Arg Pro Ala Glu Asp 1135 1140 1145	23456
5	CAG GTG GCG CTG CGG GCT TCG GGC GCG TAC GGC CGC AGG CTG GTC CGG Gln Val Ala Leu Arg Ala Ser Gly Ala Tyr Gly Arg Arg Leu Val Arg 1150 1155 1160 1165	23504
10	GCC TCC GCG GCG GGC GGC GCG GAC GGC TGG CGG CCG CGG GGA ACG GTG Ala Ser Ala Ala Gly Gly Ala Asp Gly Trp Arg Pro Arg Gly Thr Val 1170 1175 1180	23552
15	CTG GTG GTG GGC GAC ACC GCG GAG GTC GCC GGA CCG CTG GTG CGC TGG Leu Val Val Gly Asp Thr Ala Glu Val Ala Gly Pro Leu Val Arg Trp 1185 1190 1195	23600
20	CTG CTC GGC AAC GGC GCA CGG CGG GTG ACC CTG TCC GGA CTC TCC GGC Leu Leu Gly Asn Gly Ala Arg Arg Val Thr Leu Ser Gly Leu Ser Gly 1200 1205 1210	23648
25	CCG CTG CCG GAG GAA CTC GCC GAT GTG GCG GCA CGG GTG ACC CTG GCG Pro Leu Pro Glu Glu Leu Ala Asp Val Ala Ala Arg Val Thr Val Ala 1215 1220 1225	23696
30	CCC TGT GAT CCG GCC GAT CGC CCC GCC CTG CGG ACG CTG CTC GCC GAA Pro Cys Asp Pro Ala Asp Arg Pro Ala Leu Arg Thr Leu Leu Ala Glu 1230 1235 1240 1245	23744
35	CAG GCG CCG ACC GCC GTG CTC GTG GCG CCC CCG GCC GTC CCG CCC ACG Gln Ala Pro Thr Ala Val Leu Val Ala Pro Pro Ala Val Pro Pro Thr 1250 1255 1260	23792
40	CCG CTC GCG GAG ATG ACC GCC GAG GCG TTA GCC ATC GCG CTG TCC GCG Pro Leu Ala Glu Met Thr Ala Glu Ala Leu Ala Ile Ala Leu Ser Ala 1265 1270 1275	23840
45	AAG ACC GGT CTG GTC GAC CGT CTG GAC TCG CTG CTC GAC GAG CCG GAC Lys Thr Gly Leu Val Asp Arg Leu Asp Ser Leu Leu Asp Glu Pro Asp 1280 1285 1290	23888
50	CCC CTG CTC GAG GAC CGG GAA CTC GAC GCG TTC GTC GTC TTC TCC TCC Pro Leu Leu Glu Asp Gly Glu Leu Asp Ala Phe Val Val Phe Ser Ser 1295 1300 1305	23936
55	GTG GCA GGG GTG TGG GGC GGC GCG GGA CAG GGT GGT TAC GCG GCC GGT Val Ala Gly Val Trp Gly Gly Ala Gly Gln Gly Gly Tyr Ala Ala Gly 1310 1315 1320 1325	23984
	ACC GCG TAC CTC GAC GCG CTC GCC GAA TGC CGG CGG GCC GGG GGG CTG Thr Ala Tyr Leu Asp Ala Leu Ala Glu Cys Arg Arg Ala Gly Gly Leu 1330 1335 1340	24032
	CCG GTC ACC TCG GTG GCG TGG ACG CCG TGG CTC GGT ACG CCG GCG GCG Pro Val Thr Ser Val Ala Trp Thr Pro Trp Leu Gly Thr Pro Ala Ala 1345 1350 1355	24080
	GAC TCC CTG GGC GAG CAG ATG AGC CGA GCT GGC ATC ACC CCC CTG GAT Asp Ser Leu Gly Glu Gln Met Ser Arg Ala Gly Ile Thr Pro Leu Asp 1360 1365 1370	24128

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	CCG GCG GCC TCG CTG GAT GCG CTC GCC CGT GCG GTG GGC CGG CCC GCG Pro Ala Ala Ser Leu Asp Ala Leu Ala Arg Ala Val Gly Arg Arg Ala 1375 1380 1385	24176
5	GCG TGT GTG ACG GTC GCC GAC ATC GAC TGG GAG CGG TTC GCC TCC GCG Gly Cys Val Thr Val Ala Asp Ile Asp Trp Glu Arg Phe Ala Ser Ala 1390 1395 1400 1405	24224
10	TAC ACG GCC ACC CGT CCC ACG CCG ATG TTC GAC GAG GTG CCC GAG GTG Tyr Thr Ala Thr Arg Pro Thr Pro Met Phe Asp Glu Val Pro Glu Val 1410 1415 1420	24272
15	CGG CGG ATA CAG GCC GCG TGG GCG GAA GCG GAG GCC GAC GCC GCG CGC Arg Arg Ile Gln Ala Ala Trp Ala Glu Ala Glu Ala Asp Ala Ala Arg 1425 1430 1435	24320
20	AGC GGT GCC GGC GGC GAC TCG CAG CTG CTG CGC TCC CTC CGG GGC CGG Ser Gly Ala Gly Gly Asp Ser Gln Leu Leu Arg Ser Leu Arg Gly Arg 1440 1445 1450	24368
25	CCC GAG GAG GCC CAA CTG GCG GAG CTG CTG CGG CTG GTG CGC ACC CAT Pro Glu Glu Ala Gln Leu Ala Glu Leu Leu Arg Leu Val Arg Thr His 1455 1460 1465	24416
30	GCC GCC GCG GTG CTC GGC CTG GGC TCG CCC GGC GCG GTG GAG GCG CGG Ala Ala Ala Val Leu Gly Leu Gly Ser Pro Gly Ala Val Glu Ala Arg 1470 1475 1480 1485	24464
35	CGT TCG TTC AAG GAC CTG GGC TTC AAC TCG GTG ACG GCG GTG GAG CTG Arg Ser Phe Lys Asp Leu Gly Phe Asn Ser Val Thr Ala Val Glu Leu 1490 1495 1500	24512
40	CGG AAC CGG CTG AAG GAG GCG ACG GGA CTC CGG CTG GAG GTG TCC CTG Arg Asn Arg Leu Lys Glu Ala Thr Gly Leu Arg Leu Glu Val Ser Leu 1505 1510 1515	24560
45	GTC TTC GAC CAC CCG GAC CCG GCC TCC CTC GCC CGG CAT CTG CTG GAT Val Phe Asp His Pro Asp Pro Ala Ser Leu Ala Arg His Leu Leu Asp 1520 1525 1530	24608
50	CTC GCC CTC GGC CAG GAG CCG GAG GAG ACG CCG CGG GCG TTC GCG CTC Leu Ala Leu Gly Gln Glu Pro Glu Glu Thr Pro Arg Ala Phe Ala Leu 1535 1540 1545	24656
55	GAA CCC GCG CCG AAC GGG GAG CCG ATC GCG ATC GTG TCC ATG GCC TGC Glu Pro Ala Pro Asn Gly Glu Pro Ile Ala Ile Val Ser Met Ala Cys 1550 1555 1560 1565	24704
	CGT ATG CCG GGG GGT GTC AGC ACG CCC GAG GAG CTG TGG CGG CTG CTG Arg Met Pro Gly Gly Val Ser Thr Pro Glu Glu Leu Trp Arg Leu Leu 1570 1575 1580	24752
	CGG GAC GGC AAG GAC GCG ATC GGG CCG TTC CCC GCC AAC CGG GGC TGG Arg Asp Gly Lys Asp Ala Ile Gly Pro Phe Pro Ala Asn Arg Gly Trp 1585 1590 1595	24800
	GAC CTG GAG AAC CTC TAC GAC CCC GAC CCG GAC GCC GAC GGC CGC ACC Asp Leu Glu Asn Leu Tyr Asp Pro Asp Pro Ala Asp Gly Arg Thr 1600 1605 1610	24848

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	TAT GTG CGC GAG GGC GGA TTC CTC CAC GAG GCA CCG GAC TTC GAC CCC Tyr Val Arg Glu Gly Gly Phe Leu His Glu Ala Pro Asp Phe Asp Pro 1615 1620 1625	24896
5	TCG TTC TTC GGC ATC TCG CCG CGC GAG GCG CTG GCG ATG GAC CCG CAG Ser Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln 1630 1635 1640 1645	24944
10	CAG CGG CTG CTG CTG GAG ACT TCC TGG GAG GCC TTG GAG CGC GCC GGC Gln Arg Leu Leu Leu Glu Thr Ser Trp Glu Ala Leu Glu Arg Ala Gly 1650 1655 1660	24992
15	ATC GAC CCG GCG AGG CTG CGC GGC AGC CGT ACC GGC GTC TTC GTC GGG Ile Asp Pro Ala Arg Leu Arg Gly Ser Arg Thr Gly Val Phe Val Gly 1665 1670 1675	25040
20	ACG AAC GGC CAG CAC TAC ATG CCG CTG CTC CAG AAC GGC GGG GAC AGC Thr Asn Gly Gln His Tyr Met Pro Leu Leu Gln Asn Gly Gly Asp Ser 1680 1685 1690	25088
25	TTC GAC GGC TAT CTG GGC ACC GGC AAC TCG GCG AGT GTG ATG TCG GGC Phe Asp Gly Tyr Leu Gly Thr Gly Asn Ser Ala Ser Val Met Ser Gly 1695 1700 1705	25136
30	CGG CTG TCG TAC GTG TTC GGC CTC GAA GGC CCC GCC GTG ACC GTG GAC Arg Leu Ser Tyr Val Phe Gly Leu Glu Gly Pro Ala Val Thr Val Asp 1710 1715 1720 1725	25184
35	ACC GCC TGC TCG GCG TCC CTG GTG GCG CTG CAC CTG GCG GTG CAG GCG Thr Ala Cys Ser Ala Ser Leu Val Ala Leu His Leu Ala Val Gln Ala 1730 1735 1740	25232
40	ATG CGG CGC GGC GAG TGC GAC ATG GCG CTG GTC GGC GGC GCG ACG GTG Met Arg Arg Gly Glu Cys Asp Met Ala Leu Val Gly Gly Ala Thr Val 1745 1750 1755	25280
45	ATG TCG ACG CCC GAG ATG CTG GTG GAG TTC TCC CGG CAG CGG GTG ATC Met Ser Thr Pro Glu Met Leu Val Glu Phe Ser Arg Gln Arg Val Ile 1760 1765 1770	25328
50	TCC GCC AAC GGC CGG TCG AGG GCC TTC GCC GCC GGT GCC GAC GGT GTG Ser Ala Asn Gly Arg Ser Arg Ala Phe Ala Ala Gly Ala Asp Gly Val 1775 1780 1785	25376
55	GCG CTC GGC GAG GGC GTG GGC GTC CTG CTG GTG GAG CGG CTG TCG GAC Ala Leu Gly Glu Gly Val Gly Val Leu Leu Val Glu Arg Leu Ser Asp 1790 1795 1800 1805	25424
	GCC GAG CGC AAC GGC CAT CCG GTG CTG GCG GTG GTC CGC GGC TCG GCG Ala Glu Arg Asn Gly His Pro Val Leu Ala Val Val Arg Gly Ser Ala 1810 1815 1820	25472
	GTC AAC CAG GAC GGC GCC TCC AAC GGG CTG ACG GCG CCC AAC GGG CCC Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro 1825 1830 1835	25520
	TCC CAG CAG CGG GTG ATC CGG CAG GCG CTG GCG GAC GCC GGG CTG CGG Ser Gln Gln Arg Val Ile Arg Gln Ala Leu Ala Asp Ala Gly Leu Arg 1840 1845 1850	25568

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	CCC GAG GAC ATC GAC GCC GTC GAG GCG CAC CGC ACC GGC ACC GAG CTG Pro Glu Asp Ile Asp Ala Val Glu Ala His Gly Thr Gly Thr Glu Leu 1855 1860 1865	25616
5	GGC GAC CCC ATC GAG GCC GAG GCG CTG CTC GCC ACC TAT GGA AGG ACC Gly Asp Pro Ile Glu Ala Glu Ala Leu Leu Ala Thr Tyr Gly Arg Thr 1870 1875 1880 1885	25664
10	CGT ACG GCG GAC CGC CCG CTG TGG CTC GGC TCC CTG AAG TCC AAC ATC Arg Thr Ala Asp Arg Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile 1890 1895 1900	25712
15	GGG CAC ACC CAG GCC GCC GGC GTG GCG GGC GTC ATC AAG ATG GTG Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val 1905 1910 1915	25760
20	CTC GCG CTG GGC AAC GAG ACA CTG CCG CGC ACC CTG CAC GTG GAT GAG Leu Ala Leu Gly Asn Glu Thr Leu Pro Arg Thr Leu His Val Asp Glu 1920 1925 1930	25808
25	CCC ACA CCG CGC GTG GAC TGG TCC TCT GGC GCG GTC TCC CTG CTC ACC Pro Thr Pro Arg Val Asp Trp Ser Ser Gly Ala Val Ser Leu Leu Thr 1935 1940 1945	25856
30	GAG CCG GTG GAC TGG CCC GCC GGC CCG TCC GCG CCG CGC CGT GCG GCC Glu Pro Val Asp Trp Pro Ala Gly Pro Ser Ala Pro Arg Arg Ala Ala 1950 1955 1960 1965	25904
35	GTG TCC TCG TTC GGC ATC AGC GGC ACC AAC GCC CAC ACG ATC CTG GAG Val Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His Thr Ile Leu Glu 1970 1975 1980	25952
40	CAG GCC CCC GTC CCC GCG GAG TCC CGC CCC GGG ACG GAG CCG GCG GAC Gln Ala Pro Val Pro Ala Glu Ser Arg Pro Gly Thr Glu Pro Ala Asp 1985 1990 1995	26000
45	GGC ACG GGC GCG TGG GAG AAC GTG ACC GTT CCG CTG CTG CTG TCC GGC Gly Thr Gly Ala Trp Glu Asn Val Thr Val Pro Leu Leu Ser Gly 2000 2005 2010	26048
50	CAC ACC GAG GCG GCG CTG CGC GAG CAG AGC ACG AGG CTG CTG AAC GAC His Thr Glu Ala Ala Leu Arg Glu Gln Ser Thr Arg Leu Leu Asn Asp 2015 2020 2025	26096
55	CTG CTG GAG CAC CCG GAC GAG CAC CCG GCC GAC GTC GGC TAC ACC CTG Leu Leu Glu His Pro Asp Glu His Pro Ala Asp Val Gly Tyr Thr Leu 2030 2035 2040 2045	26144
	ATC ACC GGC AGG GCC CAC TTC GGG CAC CGG GCC GGC GTG ATC GGC GAG Ile Thr Gly Arg Ala His Phe Gly His Arg Ala Ala Val Ile Gly Glu 2050 2055 2060	26192
	AGC CGG GAA GAA CTG CTC GAC GCC CTG AAG GCT CTG GCC GAG GGC CGC Ser Arg Glu Glu Leu Leu Asp Ala Leu Lys Ala Leu Ala Glu Gly Arg 2065 2070 2075	26240
	GAG CAC CAC ACC GTG GTA CGG GGC GAC GGG ACG GCC CAC CCG GAC CGG Glu His His Thr Val Val Arg Gly Asp Gly Thr Ala His Pro Asp Arg 2080 2085 2090	26288

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	CGC GTG GTC TTC GTC CCC GGG CAG GGC TCG CAG TCG CCG TCG ATG Arg Val Val Phe Val Phe Pro Gly Gln Gly Ser Gln Trp Pro Ser Met 2095 2100 2105	26336
5	GCC CGG GAC CTG CTC GAC CGC GCG CCC GCC TTC CGC GAG ACG GCG AAG Ala Arg Asp Leu Leu Asp Arg Ala Pro Ala Phe Arg Glu Thr Ala Lys 2110 2115 2120 2125	26384
10	GCC TGC GAC GCC GCG CTG AGC GTC CAT CTG GAC TGG TCC GTG CTC GAT Ala Cys Asp Ala Ala Leu Ser Val His Leu Asp Trp Ser Val Leu Asp 2130 2135 2140	26432
15	GTC CTC CAG GAG AAG CCG GAC GCG CCG CTG AGC CGG GTC GAC GTG Val Leu Gln Glu Lys Pro Asp Ala Pro Pro Leu Ser Arg Val Asp Val 2145 2150 2155	26480
20	GTG CAG CCC GTG CTG TTC ACG ATG ATG CTG TCG CTC GCC GCC TGC TGG Val Gln Pro Val Leu Phe Thr Met Met Leu Ser Leu Ala Ala Cys Trp 2160 2165 2170	26528
25	CGG GAC CTC GGC GTC CAC CCG GCC GTG GTG GGC CAC TCC CAG GGA Arg Asp Leu Gly Val His Pro Ala Ala Val Val Gly His Ser Gln Gly 2175 2180 2185	26576
30	GAG ATC GCG GCG GCC TGC GTG GCC GGC GCG CTC TCC CTG GAG GAC GCG Glu Ile Ala Ala Cys Val Ala Gly Ala Leu Ser Leu Glu Asp Ala 2190 2195 2200 2205	26624
35	GCG CGG ATC GTG GCG CTG CGC AGC CGG GCA TGG CTC ACA CTG GCC GGC Ala Arg Ile Val Ala Leu Arg Ser Arg Ala Trp Leu Thr Leu Ala Gly 2210 2215 2220	26672
40	AAG GGC GGC ATG GCC GCC GTC TCC CTG CCG GAA GCC CGG CTG CGC GAG Lys Gly Gly Met Ala Ala Val Ser Leu Pro Glu Ala Arg Leu Arg Glu 2225 2230 2235	26720
45	CGG ATC GAG CGG TTC GGG CAG CGG CTG TCG GTG GCC GCG GTG AAC AGC Arg Ile Glu Arg Phe Gly Gln Arg Leu Ser Val Ala Ala Val Asn Ser 2240 2245 2250	26768
50	CCG GGC ACG GCG GCG GTC GCC GGT GAC GTG GAC GCG CTG CGG GAA CTG Pro Gly Thr Ala Ala Val Ala Gly Asp Val Asp Ala Leu Arg Glu Leu 2255 2260 2265	26816
55	CTG GCG GAG CTG ACC GCG GAG GGC ATC CGG GCC AAG CCG ATC CCC GGC Leu Ala Glu Leu Thr Ala Glu Gly Ile Arg Ala Lys Pro Ile Pro Gly 2270 2275 2280 2285	26864
	GTG GAC ACG GCC GGC CAC TCC GCG CAG GTG GAC GGC CTG AAG GAG CAT Val Asp Thr Ala Gly His Ser Ala Gln Val Asp Gly Leu Lys Glu His 2290 2295 2300	26912
	CTC TTC GAG GTG CTG GCG CCG GTC TCC CCG CGC TCC TCG GAC ATC CCG Leu Phe Glu Val Leu Ala Pro Val Ser Pro Arg Ser Ser Asp Ile Pro 2305 2310 2315	26960
	TTC TAC TCG ACG GTG ACG GGC GCG CCG CTG GAC ACC GAG CGG CTG GAC Phe Tyr Ser Thr Val Thr Gly Ala Pro Leu Asp Thr Glu Arg Leu Asp 2320 2325 2330	27008

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	GCC GGG TAC TGG TAC CGC AAC ATG CGG GAG CCC GTG GAG TTC GAG AAG Ala Gly Tyr Trp Tyr Arg Asn Met Arg Glu Pro Val Glu Phe Glu Lys 2335 2340 2345	27056
5	GCC GTC AGG GCA CTG ATC GCC GAC GGC TAC GAC CTG TTC CTG GAG TGC Ala Val Arg Ala Leu Ile Ala Asp Gly Tyr Asp Leu Phe Leu Glu Cys 2350 2355 2360 2365	27104
10	AAC CCG CAC CCG ATG CTC GCC ATG TCG CTG GAC GAG ACA CTC ACC GAC Asn Pro His Pro Met Leu Ala Met Ser Leu Asp Glu Thr Leu Thr Asp 2370 2375 2380	27152
15	AGC GGC GGC CAC GGC ACC GTG ATG CAC ACC CTC CGC CGG CAG AAG GGC Ser Gly Gly His Gly Thr Val Met His Thr Leu Arg Arg Gln Lys Gly 2385 2390 2395	27200
20	AGC GCC AAG GAC TTC GGC ATG GCG CTC TGC CTC GCC TAT GTC AAC GGA Ser Ala Lys Asp Phe Gly Met Ala Leu Cys Leu Ala Tyr Val Asn Gly 2400 2405 2410	27248
25	CTG GAG ATC GAC GGA GAA GCC CTC TTC GGC CCC GAC TCA CGC CGG GTG Leu Glu Ile Asp Gly Glu Ala Leu Phe Gly Pro Asp Ser Arg Arg Val 2415 2420 2425	27296
30	AAC CCG CCG ACG TAC CCG TTC CAG CGG GAG CGC TAC TGG TAC CAC CCC Asn Pro Pro Thr Tyr Pro Phe Gln Arg Glu Arg Tyr Trp Tyr His Pro 2430 2435 2440 2445	27344
35	ACG AGC GGC AGG CGC GGC GAC ATC ACG GCG GCC GGC GTG GCC GAG GCG Thr Ser Gly Arg Arg Gly Asp Ile Thr Ala Ala Gly Val Ala Glu Ala 2450 2455 2460	27392
40	GAG CAC CCG CTG CTC GGC GCC GGC GTC GAA CTC CCG GAG ACC GGG GGC Glu His Pro Leu Leu Gly Ala Gly Val Glu Leu Pro Glu Thr Gly Gly 2465 2470 2475	27440
45	ACG GTG TAC ACC GCG CGG TTC GGC CCG GAC AGC CGG CCG TGG CTG GCC Thr Val Tyr Thr Ala Arg Phe Gly Pro Asp Ser Arg Pro Trp Leu Ala 2480 2485 2490	27488
50	GAC CAC GCG CTG CTG GGC ACC GTG CTG CTG CCC GGC ACG GCA ATC CTG Asp His Ala Leu Leu Gly Thr Val Leu Leu Pro Gly Thr Ala Ile Leu 2495 2500 2505	27536
55	GAC CTG GTG CTG TGG GCG GGC GAA CGC TCC GGC TGC GGC CGC GTC GGT Asp Leu Val Leu Trp Ala Gly Glu Arg Ser Gly Cys Gly Arg Val Gly 2510 2515 2520 2525	27584
	GAA CTG CCG CTC CAG GCA CCG CTG GTC CTG CCG GAC AGC GGC GAC GTC Glu Leu Ala Leu Gln Ala Pro Leu Val Leu Pro Asp Ser Gly Asp Val 2530 2535 2540	27632
	GAA CTG CGG CTG CTG GTC GGC GGC CCG GAC GAG GAG AAA CGG CGC ACC Glu Leu Arg Leu Leu Val Gly Gly Pro Asp Glu Glu Lys Arg Arg Thr 2545 2550 2555	27680
	GTC ACC GTG CAC GCG CGG CCC GCG GCG GCC GGC GGC GAG GCG CCG TGG Val Thr Val His Ala Arg Pro Ala Ala Gly Ala Glu Ala Pro Trp 2560 2565 2570	27728

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	ACC CGG CAC GCC GAA GCC GTG GTG CTG CCC GCC ACC GGC GAG GAG CCG Thr Arg His Ala Glu Ala Val Val Leu Pro Ala Thr Gly Glu Glu Pro 2575 2580 2585	27776
5	ACC CCC GCC CCG CGC CCC GTC CCC GAG CCG GCG GGC ACC ACG GAC CCC Thr Pro Ala Pro Arg Pro Val Pro Glu Pro Ala Gly Thr Thr Asp Pro 2590 2595 2600 2605	27824
10	GCC GCG TTC TAC GCG GAG TTC GCC GAG CGC GGC TAC GAC TAC GGC CCG Ala Ala Phe Tyr Ala Glu Phe Ala Glu Arg Gly Tyr Asp Tyr Gly Pro 2610 2615 2620	27872
15	GCC TTC CAG GGC TTC ACC GCC GGA GCG CGC CAC GGC GAG GAC GTC GTC Ala Phe Gln Gly Phe Thr Ala Gly Ala Arg His Gly Glu Asp Val Val 2625 2630 2635	27920
20	GCC GAG GTG GCG CTG CCC AGC GGC CTG GTG GCG GAC GCC CGT CAC CAC Ala Glu Val Ala Leu Pro Ser Gly Leu Val Ala Asp Ala Arg His His 2640 2645 2650	27968
25	CGG CTG CAC CCG GCG CTG CTC GAC GCC GCG CTC CAG GCG ATG ATC CTC Arg Leu His Pro Ala Leu Leu Asp Ala Ala Leu Gln Ala Met Ile Leu 2655 2660 2665	28016
30	GGC ACG TTC TTT GCC GAC GAC GGC CGC GCC CGG ATG CCG TTC GCG GTG Gly Thr Phe Phe Ala Asp Asp Gly Arg Ala Arg Met Pro Phe Ala Val 2670 2675 2680 2685	28064
35	CGC GGA GTA CGG CTG CAC ACG GCC GGC GAC CGG CTG CGC GTC CTG Arg Gly Val Arg Leu His Thr Ala Gly Ala Asp Arg Leu Arg Val Leu 2690 2695 2700	28112
40	ATC TCC CCG GCG GGC GAC GAG ACC GTA CGG CTG CTC TGC ACC GAC CTC Ile Ser Pro Ala Gly Asp Glu Thr Val Arg Leu Leu Cys Thr Asp Leu 2705 2710 2715	28160
45	GCG ACC GGC GCC CCC GTG CTG GAG ATC GAC GAA CTG GTC GTC CGC CCG Ala Thr Gly Ala Pro Val Leu Glu Ile Asp Glu Leu Val Val Arg Pro 2720 2725 2730	28208
50	GTG TCC GGC GAG CAG TTG GCG GGC GGC GGC CCG CGC AAC GGC GGC Val Ser Gly Glu Gln Leu Ala Ala Gly Ala Pro Gly Arg Asn Gly Gly 2735 2740 2745	28256
55	GAG CTG TAC CGG GTC GAC TGG ACG GTG CTG CCG GAG CCC GCC GAG GTG Glu Leu Tyr Arg Val Asp Trp Thr Val Leu Pro Glu Pro Ala Glu Val 2750 2755 2760 2765	28304
	CCC GCG CCG CGC TGG GCC CTC CTC GGC GAG GAC CAC GCC GGC CTG GCC Pro Ala Pro Arg Trp Ala Leu Leu Gly Glu Asp His Ala Gly Leu Ala 2770 2775 2780	28352
	GAT GTG CTC GGA GGG ACG GGC GGC TGC GAG CGG TAC GAC ACC CTC Asp Val Leu Gly Gly Thr Gly Gly Cys Glu Arg Tyr Asp Thr Leu 2785 2790 2795	28400
	ACC GGC CTG CTG GAG GCC ACC ACC CGG TCG GCC GGC GGA ATC CTG CCC Thr Gly Leu Leu Glu Ala Thr Thr Arg Ser Ala Gly Gly Ile Leu Pro 2800 2805 2810	28448

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	GAC ATC GTC GCG CTC TCC TTG CCC ACC GCC CCG GAG CCC GGC CCC CAG Asp Ile Val Ala Leu Ser Leu Pro Thr Ala Pro Glu Pro Gly Pro Gln 2815 2820 2825	28496
5	GCG GTG CGC GAG GTG CTG TCC CAG GCG CTC GAC GCC GCC CAG GCG TGG Ala Val Arg Glu Val Leu Ser Gln Ala Leu Asp Ala Ala Gln Ala Trp 2830 2835 2840 2845	28544
10	CTG GCC GCC GGC GCC GAG ACC GCC TCC GCC CGG CTG GTG TTC GTC ACC Leu Ala Ala Gly Ala Glu Thr Ala Ser Ala Arg Leu Val Phe Val Thr 2850 2855 2860	28592
15	GCG GGC GCG GTG GCC ACC ACG GCG GAA ACC GTG CGC GAC ATC GCG Gly Gly Ala Val Ala Thr Thr Ala Asp Glu Thr Val Arg Asp Ile Ala 2865 2870 2875	28640
20	GCG GCC GCC GTC TGG GGC CTG GTC CGC TCG GCG CAG TCC GAG GAA CCC Ala Ala Ala Val Trp Gly Leu Val Arg Ser Ala Gln Ser Glu Glu Pro 2880 2885 2890	28688
25	GAC CGC ATG GTC CTG CTC GAC CTG GAC GGC GAG CGG CCC ACC GCG CGG Asp Arg Met Val Leu Leu Asp Leu Asp Gly Glu Arg Pro Thr Ala Arg 2895 2900 2905	28736
30	ACG CTG GCG GCG CTC GCG TCC GGC GAA CCG CAA CTC GCC GTG CGC Thr Leu Ala Ala Ala Leu Ala Ser Gly Glu Pro Gln Leu Ala Val Arg 2910 2915 2920 2925	28784
35	GGC TCC ACG GTG GCC GCT CCC CGG CTG GCC CCG GCC GGG CCC GGC CCG Gly Ser Thr Val Ala Ala Pro Arg Leu Ala Pro Ala Gly Pro Gly Pro 2930 2935 2940	28832
40	GAG GAC CTC GTA CCG CCC GCC GGC ACC ACC GCC TGG CGG CTC ACC CCC Glu Asp Leu Val Pro Pro Ala Gly Thr Thr Ala Trp Arg Leu Thr Pro 2945 2950 2955	28880
45	GGC GGG GGG ACG CTG GAG GAA CTG TCG CTC GCG CCC GCC CCC GAC GCG Gly Gly Gly Thr Leu Glu Glu Leu Ser Leu Ala Pro Ala Pro Asp Ala 2960 2965 2970	28928
50	GAG GAA CCA CTG GCA CCG GCC CAG GTA CGC ATC GCC GTC CGC GCG GCG Glu Glu Pro Leu Ala Pro Gly Gln Val Arg Ile Ala Val Arg Ala Ala 2975 2980 2985	28976
55	GGC GTG AAC TTC CGC GAC GCC CTG ATC GCC CTC GGC ATG TAC CCG GGC Gly Val Asn Phe Arg Asp Ala Leu Ile Ala Leu Gly Met Tyr Pro Gly 2990 2995 3000 3005	29024
	AAG GGA ACC ATG GGC GCC GAG GGA GCC GGC GTC GTC GTC GAG ACC GCC Lys Gly Thr Met Gly Ala Glu Gly Ala Gly Val Val Val Glu Thr Ala 3010 3015 3020	29072
	CCC GAT GTC ACC GGC CTC TCC GCC GGA GAC CGC GTG CTC GGC ATG TGG Pro Asp Val Thr Gly Leu Ser Ala Gly Asp Arg Val Leu Gly Met Trp 3025 3030 3035	29120
	AAC GGC GGC TTC GGG CCC CTC GTG GTG GCC GAC CAC CGC ATG GTG GCC Asn Gly Gly Phe Gly Pro Leu Val Val Ala Asp His Arg Met Val Ala 3040 3045 3050	29168

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	CCG ATC CCC CAC GGC TGG TCG TAC GCC GAG GCG GCC TCC GTG CCC GCC Pro Ile Pro His Gly Trp Ser Tyr Ala Glu Ala Ala Ser Val Pro Ala 3055 3060 3065	29216
5	GTC CTC CTC ACC TCC TAC TAC GCG CTG ACC CGG CTG GCC CGG GCC CGC Val Leu Leu Thr Ser Tyr Tyr Ala Leu Thr Arg Leu Ala Arg Ala Arg 3070 3075 3080 3085	29264
10	ACC GGA CAG ACC GTC CTC GTC CAC GCC GCC GGC GGT GTC GGC ATG Thr Gly Gln Thr Val Leu Val His Ala Ala Gly Gly Val Gly Met 3090 3095 3100	29312
15	GCG ACC CTC CAA CTC GCC CGC CAC CTC GGC CTG GAG GTG TAC GCC ACC Ala Thr Leu Gln Leu Ala Arg His Leu Gly Leu Glu Val Tyr Ala Thr 3105 3110 3115	29360
20	GCG AGC ACC GGC AAA TGG GAC GCC CTG CAG AAG CAC GGC ATC CCC GAC Ala Ser Thr Gly Lys Trp Asp Ala Leu Gln Lys His Gly Ile Pro Asp 3120 3125 3130	29408
25	GAC CGC ATC GCC GAC TCC CGC ACC CTG GAC TTC GCC GAG CGC TTC CTG Asp Arg Ile Ala Asp Ser Arg Thr Leu Asp Phe Ala Glu Arg Phe Leu 3135 3140 3145	29456
30	TCC CGG ACG GGC CGG GGT GTC GAC ATC GTG CTG AAC TCC CTG GCC Ser Arg Thr Gly Arg Gly Val Asp Ile Val Leu Asn Ser Leu Ala 3150 3155 3160 3165	29504
35	GCG GAG TTC GTC GAC GCC TCA CTG CGG CTG CCG CGC GGC GGG CAC Gly Glu Phe Val Asp Ala Ser Leu Arg Leu Leu Pro Arg Gly Gly His 3170 3175 3180	29552
40	TTC CTG GAA CTC GGC AAG GCC GAC GTC CGC GAC CCC CGG CGG ATC GCC Phe Leu Glu Leu Gly Lys Ala Asp Val Arg Asp Pro Arg Arg Ile Ala 3185 3190 3195	29600
45	GCC GCC CAT CCG GGC ACC GAC TAC CGG GCG TTC GAC CTG GTG CAG GCC Ala Ala His Pro Gly Thr Asp Tyr Arg Ala Phe Asp Leu Val Gln Ala 3200 3205 3210	29648
50	GGT CCC GAC ACC GTC GGG GAG ATG CTC GGG GAA CTG CTG GAA CTG TTC Gly Pro Asp Thr Val Gly Glu Met Leu Gly Glu Leu Leu Glu Leu Phe 3215 3220 3225	29696
55	GCG GCC GGA GCG CTG CGC CCG CTG CCG CTC ACC GCC TAC GGC ATA CGC Ala Ala Gly Ala Leu Arg Pro Leu Pro Leu Thr Ala Tyr Gly Ile Arg 3230 3235 3240 3245	29744
	GAC GCC CGC ACC GCC TTG CGC ACC CTC AGC CAG GCC CGG CAC ACC GGC Asp Ala Arg Thr Ala Leu Arg Thr Leu Ser Gln Ala Arg His Thr Gly 3250 3255 3260	29792
	AAG CTC GTG CTG ACG GTG CCT GCC GGA TTC GAC ACC CAC CGC ACG GTG Lys Leu Val Leu Thr Val Pro Ala Gly Phe Asp Thr His Arg Thr Val 3265 3270 3275	29840
	CTC CTC ACC GGC GGC ACG GGC ACG CTC GGC CAG ACA CTC GCC CGC CAT Leu Leu Thr Gly Gly Thr Gly Thr Leu Gly Gln Thr Leu Ala Arg His 3280 3285 3290	29888

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	CTG GTC AAC CGC CAC GGC GTA CGG CAC CTG CTG CTC GCC GGC CGC ACC Leu Val Asn Arg His Gly Val Arg His Leu Leu Leu Ala Gly Arg Thr 3295 3300 3305	29936
5	GGC GCG GCG GCC GAG GGC GTC GCG GAA CTG ATT GGT GAA CTG GGC GAG Gly Ala Ala Ala Glu Gly Val Ala Glu Leu Ile Gly Glu Leu Gly Glu 3310 3315 3320 3325	29984
10	TTG GGC GCC GAG GTC CGG GTC GCG GCC TGC GAC GCG GCC GAC CGG CAG Leu Gly Ala Glu Val Arg Val Ala Ala Cys Asp Ala Ala Asp Arg Gln 3330 3335 3340	30032
15	CGG CTC ACC GAA CTC CTC GCC GGA ATC CCC GTC GAG CAC CCG CTC GGC Arg Leu Thr Glu Leu Leu Ala Gly Ile Pro Val Glu His Pro Leu Gly 3345 3350 3355	30080
20	GCC GTC GTC CAC GCC GCG GGC ACC CTC GAC GAC GGC ACC ATC CCC TCA Ala Val Val His Ala Ala Gly Thr Leu Asp Asp Gly Thr Ile Pro Ser 3360 3365 3370	30128
25	CTG ACC GGC GAG AAC ATC GAC AAC GTG CTG CGG CCC AAG GCC GAC GCC Leu Thr Gly Glu Asn Ile Asp Asn Val Leu Arg Pro Lys Ala Asp Ala 3375 3380 3385	30176
30	GTG CTC AAC CTG CAC GAG CTG ACC CGC GAC GGC GAC CTC TCG GCG TTC Val Leu Asn Leu His Glu Leu Thr Arg Asp Ala Asp Leu Ser Ala Phe 3390 3395 3400 3405	30224
35	GTC CTC TAC TCG TCC TCC TCG GCG CTG CTC GGC AGC CCC GGC CAG GGC Val Leu Tyr Ser Ser Ser Ala Leu Leu Gly Ser Pro Gly Gln Gly 3410 3415 3420	30272
40	GCC TAC GCC GCG GCC AAC GCC TTC CTG GAC GGC TTC GCC CGA TAC CGC Ala Tyr Ala Ala Ala Asn Ala Phe Leu Asp Gly Phe Ala Arg Tyr Arg 3425 3430 3435	30320
45	AAG GGC CTC GGG CTG CCG GCG CTC TCG CTG GCC TGG GGA CTG TGG GGC Lys Gly Leu Gly Leu Pro Ala Leu Ser Leu Ala Trp Gly Leu Trp Gly 3440 3445 3450	30368
50	AGC AAC AGC CGC ATG GCG GGC CAC CTC GAC CAG TCG GGC ATG CAA CGG Ser Asn Ser Arg Met Ala Gly His Leu Asp Gln Ser Gly Met Gln Arg 3455 3460 3465	30416
55	CGC CTG AAC CGG AGC GGC ATC ATG GCG CTC ACC GAC GCC GAG GGC CTC Arg Leu Asn Arg Ser Gly Ile Met Ala Leu Thr Asp Ala Glu Gly Leu 3470 3475 3480 3485	30464
	GCC CTG TTC GAC GCC GCA CAG GAC GGC GGG GAC GCG CTG CTG GTG CCG Ala Leu Phe Asp Ala Ala Gln Asp Gly Gly Asp Ala Leu Leu Val Pro 3490 3495 3500	30512
	ATG CGG CTC AAC CGG ACG GCC CTT CGC GCC TCG GGA CGG ATC ACC CCG Met Arg Leu Asn Arg Thr Ala Leu Arg Ala Ser Gly Arg Ile Thr Pro 3505 3510 3515	30560
	TTC CTC AGC GGC TTG GCC GGC GGG CCG GCG GCG GGG GAG AGG CGC Phe Leu Ser Gly Leu Ala Gly Gly Pro Ala Ala Gly Glu Arg Arg 3520 3525 3530	30608

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	CCC GAG GTG GCA GCC GTA TCC GGG ACA CTC CGC GAA CGG CTG ACC GGG Pro Glu Val Ala Ala Val Ser Gly Thr Leu Ala Glu Arg Leu Thr Gly 3535 3540 3545	30656
5	CTC ACG GCA CAG GAA GGG CAC GCC CTC GTC CTG GCC GAG ATC CGC GCC Leu Thr Ala Gln Glu Gly His Ala Leu Val Leu Ala Glu Ile Arg Ala 3550 3555 3560 3565	30704
10	CAC GCG GCG GCG GTG CTG GGC CAC GGC TCC GAC GAC TCG ATC CCC GAG His Ala Ala Ala Val Leu Gly His Gly Ser Asp Asp Ser Ile Pro Glu 3570 3575 3580	30752
15	GAC CGG GCC TTC AAG GAC CTC GGC TTC GAC TCG CTC ACC GCC GTG GAG Asp Arg Ala Phe Lys Asp Leu Gly Phe Asp Ser Leu Thr Ala Val Glu 3585 3590 3595	30800
20	ATG CGC AAC CGG CTG AGC GCG GCC ACC GGC CTC CGG CTG CCC GCC ACC Met Arg Asn Arg Leu Ser Ala Ala Thr Gly Leu Arg Leu Pro Ala Thr 3600 3605 3610	30848
25	CTC GTC TTC GAC CAC CCG ACC CCG GGC GAG CTG GCC GGC CAC CTG AGT Leu Val Phe Asp His Pro Thr Pro Gly Glu Leu Ala Gly His Leu Ser 3615 3620 3625	30896
30	GCT GAA CTG TCC GCC GAC GAT GCC CCG GGC AGC GCC TCC CCG CTT ACC Ala Glu Leu Ser Ala Asp Asp Ala Pro Gly Ser Ala Ser Pro Leu Thr 3630 3635 3640 3645	30944
35	GAA CTC GAC CGT TTC GAA GCC CTG TTC ACC GCT CTC GCA CCG GGG ACC Glu Leu Asp Arg Phe Glu Ala Leu Phe Thr Ala Leu Ala Pro Gly Thr 3650 3655 3660	30992
40	ACC AAG GAC ACC CCG GGC GGG GCC GGG GCA CTG ATG ATC GAC GAG GCC Thr Lys Asp Thr Pro Gly Gly Ala Gly Ala Leu Met Ile Asp Glu Ala 3665 3670 3675	31040
45	GAG CGC CAA GAG ATC GCC GGG CGG CTC GCG GCG CTG GCC GGT CTG TGG Glu Arg Gln Glu Ile Ala Gly Arg Leu Ala Ala Leu Ala Gly Leu Trp 3680 3685 3690	31088
50	AAC CGG CTG CAC GGC ACC ACG ACG GCT CCT GAG GAC GGC GAC ACC GTC Asn Arg Leu His Gly Thr Thr Thr Ala Pro Glu Asp Gly Asp Thr Val 3695 3700 3705	31136
55	GCG GAC GCC CTG GAA GCC GCG GAC GAC CAC GAG ATC TTC GCA TTC CTC Ala Asp Ala Leu Glu Ala Ala Asp Asp His Glu Ile Phe Ala Phe Leu 3710 3715 3720 3725	31184
	GAC GAG CGG TTC TGA GCCCCCCCCA GCGACAGCAC AGCTAAAAAC AC ATG GCC Asp Glu Arg Phe * Met Ala 3730 1	31237
	AAC GCG AAC GAG CAG CAA CTC CGT GCC TAT CTG AAG CGA GCG ACG ACC Asn Ala Asn Glu Gln Gln Leu Arg Ala Tyr Leu Lys Arg Ala Thr Thr 5 10 15	31285
	GAA CTC CAC CGT ACC TCC GAA CAA CTG AGG GAG GAG CGG GCA CGG GCC Glu Leu His Arg Thr Ser Glu Gln Leu Arg Glu Glu Arg Ala Arg Ala 20 25 30	31333

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	CAC GAG CCG ATC GCC GTC GTC GGC ATG GCC TGC CGC TAC CCC GGA GGC His Glu Pro Ile Ala Val Val Gly Met Ala Cys Arg Tyr Pro Gly Gly 35 40 45 50	31381
5	GCG AAC ACC CCC GAA CAG TTC TGG GAA CTG CTC GAC ACC GGC ACC GAC Ala Asn Thr Pro Glu Gln Phe Trp Glu Leu Leu Asp Thr Gly Thr Asp 55 60 65	31429
10	GCC GCC GCG CCG ATG CCC TCC GAC CGG GGA TGG GAC ACC CAC GGG CTG Ala Ala Ala Pro Met Pro Ser Asp Arg Gly Trp Asp Thr His Gly Leu 70 75 80	31477
15	TAC GAC CCC GAC CCG GCG GCA GCG GGG CGC ACC TAC TGC CGG GAG GGC Tyr Asp Pro Asp Pro Ala Ala Gly Arg Thr Tyr Cys Arg Glu Gly 85 90 95	31525
20	GGC TTC CTC CAC GAC GCG GGC GAC TTC GAC GCG GAC TTC TTC GGG ATT Gly Phe Leu His Asp Ala Gly Asp Phe Asp Ala Asp Phe Phe Gly Ile 100 105 110	31573
25	TCG CCG CGT GAG GCG GTG GCG ATG GAT CCG CAG CAG CGG CTG TTG CTG Ser Pro Arg Glu Ala Val Ala Met Asp Pro Gln Gln Arg Leu Leu Leu 115 120 125 130	31621
30	GAG ACC TCC TGG GAG GCG ATC GAA GCG GCC GGT ATC GAC CCG CGA GGA Glu Thr Ser Trp Glu Ala Ile Glu Ala Ala Gly Ile Asp Pro Arg Gly 135 140 145	31669
35	CTC CGC GGC AGC CGC ACC GGG GTG TAC GTG GGC GCC TGG GAC AGC GGC Leu Arg Gly Ser Arg Thr Gly Val Tyr Val Gly Ala Trp Asp Ser Gly 150 155 160	31717
40	TAC ACC GGC CAG GCG CAC GCG CCC TCG GCC GAG TTG GAG GCC GAC CTG Tyr Thr Gly Gln Ala His Ala Pro Ser Ala Glu Leu Glu Ala Asp Leu 165 170 175	31765
45	CTG ACC GGC GTC GTC AGC TTC ACC TCC GGC CGT ATC GCC TAC ACG Leu Thr Gly Gly Val Val Ser Phe Thr Ser Gly Arg Ile Ala Tyr Thr 180 185 190	31813
50	CTG GGG CTG GAG GGT CCG GCC TTG ACC GTG GAC ACC GCG TGT TCG TCG Leu Gly Leu Glu Gly Pro Ala Leu Thr Val Asp Thr Ala Cys Ser Ser 195 200 205 210	31861
55	TCG CTG GTC GCC CTG CAC AAC GCG GCG CAG GCG CTG CGG CGC GGC GAA Ser Leu Val Ala Leu His Asn Ala Ala Gln Ala Leu Arg Arg Gly Glu 215 220 225	31909
	TGC GAC CTG GCG TTG GCC GGT GTG ACG GTG ATG GCG ACC CCG GCG Cys Asp Leu Ala Leu Ala Gly Val Thr Val Met Ala Thr Pro Ala 230 235 240	31957
	GTG TTC GTC CAG TTC GCC CCG CAG CGA GGG CTG GCG CCG GAC GGC CGC Val Phe Val Gln Phe Ala Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg 245 250 255	32005
	TGC AAG GCG TTC GCC GAC GCC GAC GGC TTC GGC CCC GCC GAG GGT Cys Lys Ala Phe Ala Asp Ala Ala Asp Gly Phe Gly Pro Ala Glu Gly 260 265 270	32053

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	GTG GGG ATG GTG CTG GTG GAC CGG TTG TCG GAT GCC CGG CGG TTG GGG Val Gly Met Val Leu Val Glu Arg Leu Ser Asp Ala Arg Arg Leu Gly 275 280 285 290	32101
5	CAT CCG GTG TTG GCG GTG GTG TGT GGG TCG GCG GTG AAT CAG GAC GGT His Pro Val Leu Ala Val Val Cys Gly Ser Ala Val Asn Gln Asp Gly 295 300 305	32149
10	GCG TCG AAT GGT TTG ACG GCG CCG AGT GGT CCG TCG CAG GAG CGG GTG Ala Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ser Gln Glu Arg Val 310 315 320	32197
15	ATT CGT CAG GCG TTG GGG AAT GCG CGG TTG ACG GTG GCG GAT GTG GAT Ile Arg Gln Ala Leu Gly Asn Ala Arg Leu Thr Val Ala Asp Val Asp 325 330 335	32245
20	GTG GTG GAG GCG CAT GGG ACG GGG ACG CGG CTG GGT GAT CCG ATC GAG Val Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu 340 345 350	32293
25	GCG CAG GCG TTG CTG GGG ACG TAT GGG CGG GAT CGT GAT GGT GGG CGT Ala Gln Ala Leu Leu Gly Thr Tyr Gly Arg Asp Arg Asp Gly Gly Arg 355 360 365 370	32341
30	CCG GTG TGG TTG GGG TCG TTG AAG TCG AAT ATT GGT CAT GCT CAG GCG Pro Val Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln Ala 375 380 385	32389
35	GCT GCG GGG GTG GCT GGT GTG ATC AAG ATG GTG TTG GCG ATG CGG TAT Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Met Arg Tyr 390 395 400	32437
40	GGG TGG TTG CCG CGG ACG TTG CAT GTG GAT GAG CCG AGC CGG CAT GTG Gly Trp Leu Pro Arg Thr Leu His Val Asp Glu Pro Ser Arg His Val 405 410 415	32485
45	GAC TGG TCG GCT GGT GTG CGG TTG CTG ACC GAG GCG CGG GAG TGG Asp Trp Ser Ala Gly Gly Val Arg Leu Leu Thr Glu Ala Arg Glu Trp 420 425 430	32533
50	CCG GGG GTG GAC CGG CCG CGT CGG GCG GTC TCC GCC TTT GGT GTC Pro Gly Val Asp Arg Pro Arg Arg Ala Ala Val Ser Ala Phe Gly Val 435 440 445 450	32581
55	AGT GGT ACC AAC GCC CAT CTG ATC CTC GAA GCC CCC GAC ACC GCC GAG Ser Gly Thr Asn Ala His Leu Ile Leu Glu Ala Pro Asp Thr Ala Glu 455 460 465	32629
60	GCG GAG AGC GCC ACC CCG CGC GTC CGC TCT GAG GTG TCG GAG TCT GCT Ala Glu Ser Ala Thr Thr Pro Val Arg Ser Glu Val Ser Glu Ser Ala 470 475 480	32677
65	CCG GTC CTC GAT GCC CGC ACT GGT GTG GTG CCG GTG GTG GTT TCG GGG Ala Val Leu Asp Ala Arg Ser Gly Val Val Pro Val Val Val Ser Gly 485 490 495	32725
70	CGT TCG CGG GTG GTG CGG GAG GCT GCG GGC CGG TTG GCG GAG GTG Arg Ser Arg Val Val Val Arg Glu Ala Ala Gly Arg Leu Ala Glu Val 500 505 510	32773

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	GTG GAG GCC GGT GGT CTG GGG CTG GCG GAT GTG GCG GTG ACG ATG GCG Val Glu Ala Gly Gly Val Gly Leu Ala Asp Val Ala Val Thr Met Ala 515 520 525 530	32821
5	GGC CGG TCG CGG TTT GGG TAT CGG GCG GTT GTG CTG GCT CGG GGT GAG Gly Arg Ser Arg Phe Gly Tyr Arg Ala Val Val Leu Ala Arg Gly Glu 535 540 545	32869
10	GCT GAG CTT GCC GGG CGT TTG CGG GCG TTG GCG GGG GGT GAT CCG GAC Ala Glu Leu Ala Gly Arg Leu Arg Ala Leu Ala Gly Gly Asp Pro Asp 550 555 560	32917
15	GCG GGT GTG GTC ACG GGT GCG GTG GAC CCG GAG ACG GGG TCC GGT Ala Gly Val Val Thr Gly Ala Val Val Asp Pro Glu Thr Gly Ser Gly 565 570 575	32965
20	GGT GGG GGG GTG GTG TTG GTT TTC CCT GGT CAG GGG ACG CAG TGG GTG Gly Gly Gly Val Val Leu Val Phe Pro Gly Gln Gly Thr Gln Trp Val 580 585 590	33013
25	GGG ATG GGT GCG GGG CTG CTG GGG TCT TCG GAG GTG TTT GCG GCG TCG Gly Met Gly Ala Gly Leu Leu Gly Ser Ser Glu Val Phe Ala Ala Ser 595 600 605 610	33061
30	ATG CGG GAG TGT GCG CGG GCG CTG AGT GTT CAT GTG GGG TGG GAT TTG Met Arg Glu Cys Ala Arg Ala Leu Ser Val His Val Gly Trp Asp Leu 615 620 625	33109
35	CTG GAG GTG GTG TCG GGC GGG GCC GGG TTG GAG CGG GTG GAT GTG GTG Leu Glu Val Val Ser Gly Gly Ala Gly Leu Glu Arg Val Asp Val Val 630 635 640	33157
40	CAG CCG GTG ACG TGG GCG GTG ATG GTG TCG CTG GCC CGG TAC TGG CAG Gln Pro Val Thr Trp Ala Val Met Val Ser Leu Ala Arg Tyr Trp Gln 645 650 655	33205
45	GCG ATG GGT GTG GAC GTG GCT GCG GTG GTG GGT CAT TCC CAG GGG GAG Ala Met Gly Val Asp Val Ala Ala Val Val Gly His Ser Gln Gly Glu 660 665 670	33253
50	ATC GCT GCT GCC ACG GTG GCG GGG GCG TTG TCG CTG GAG GAT GCG GCG Ile Ala Ala Ala Thr Val Ala Gly Ala Leu Ser Leu Glu Asp Ala Ala 675 680 685 690	33301
55	GCT GTG GTC GCT CTG CGG GCG GGG TTG ATT GGC CGG TAT CTG GCG GGT Ala Val Val Ala Leu Arg Ala Gly Leu Ile Gly Arg Tyr Leu Ala Gly 695 700 705	33349
	CGT GGT GCG ATG GCG GCT GTT CCG CTG CCT GCC GGC GAG GTC GAG GCG Arg Gly Ala Met Ala Ala Val Pro Leu Pro Ala Gly Glu Val Glu Ala 710 715 720	33397
	GGG CTG GCG AAG TGG CCG GGT GTG GAG GTC GCG GCG GTC AAC GGT CCG Gly Leu Ala Lys Trp Pro Gly Val Glu Val Ala Ala Val Asn Gly Pro 725 730 735	33445
	GGC TCT ACG GTG GTT TCC GGG GAT CGG CGG GCG GTG GCC GGT TAT GTG Ala Ser Thr Val Val Ser Gly Asp Arg Arg Ala Val Ala Gly Tyr Val 740 745 750	33493

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	GCC GTC TGT CAG GCG GAG GGT GTG CAG GCT CGG TTG ATA CCG GTG GAC Ala Val Cys Gln Ala Glu Gly Val Gln Ala Arg Leu Ile Pro Val Asp 755 760 765 770	33541
5	TAC GCC TCT CAC TCC CGC CAT GTG GAG GAC CTG AAG GGC GAG TTG GAG Tyr Ala Ser His Ser Arg His Val Glu Asp Leu Lys Gly Glu Leu Glu 775 780 785	33589
10	CGG GTG CTG TCC GGT ATC CGC CCC CGC AGT CCG CGG GTG CCG GTG TGT Arg Val Leu Ser Gly Ile Arg Pro Arg Ser Pro Arg Val Pro Val Cys 790 795 800	33637
15	TCC ACC GTC GCC GGA GAG CAG CCG GGC GAG CCG GTT TTC GAT GCG GGG Ser Thr Val Ala Gly Glu Gln Pro Gly Glu Pro Val Phe Asp Ala Gly 805 810 815	33685
20	TAT TGG TTC CGT AAT CTG CGG AAC CGG GTT GAG TTC TCC GCG GTG GTC Tyr Trp Phe Arg Asn Leu Arg Asn Arg Val Glu Phe Ser Ala Val Val 820 825 830	33733
25	GGT GGT TTG TTG GAG GAG GGC CAC CGT CGG TTC ATC GAG GTC AGT GCC Gly Gly Leu Leu Glu Glu Gly His Arg Arg Phe Ile Glu Val Ser Ala 835 840 845 850	33781
30	CAC CCG GTA CTC GTC CAT GCC ATT GAG CAG ACG GCC GAG GCC GCG GAC His Pro Val Leu Val His Ala Ile Glu Gln Thr Ala Glu Ala Ala Asp 855 860 865	33829
35	CGG AGT GTC CAT GCC ACC GGG ACC CTG CGC CGC CAG GAC GAC AGC CCG Arg Ser Val His Ala Thr Gly Thr Leu Arg Arg Gln Asp Asp Ser Pro 870 875 880	33877
40	CAC CGC CTG CTG ACC TCC ACC GCC GAG GCC TGG GCC CAC GGC GCC ACC His Arg Leu Leu Thr Ser Thr Ala Glu Ala Trp Ala His Gly Ala Thr 885 890 895	33925
45	CTC ACC TGG GAC CCC GCC CTG CCC CCA GGC CAC CTC ACC ACC CTC CCC Leu Thr Trp Asp Pro Ala Leu Pro Pro Gly His Leu Thr Thr Leu Pro 900 905 910	33973
50	ACC TAC CCC TTC AAC CAC CAC CAC TAC TGG CTC GAC ACC ACC CCC ACC Thr Tyr Pro Phe Asn His His Tyr Trp Leu Asp Thr Thr Pro Thr 915 920 925 930	34021
55	ACC CCC GCG ACG ACC ACC CAG AGC CCC ACC GAT GCC TGG CGC TAC CGC Thr Pro Ala Thr Thr Gln Ser Pro Thr Asp Ala Trp Arg Tyr Arg 935 940 945	34069
	GTC ACC TGG AAA GCC CTG ACC GAA GAA TCC ACT CCG GCC TCG TCC CCC Val Thr Trp Lys Ala Leu Thr Glu Glu Ser Thr Pro Ala Ser Ser Pro 950 955 960	34117
	TCC GGT CAC TGG CTC CTC GTC ACA CCC CCG ACC CCC GAA GGC CGC ACG Ser Gly His Trp Leu Leu Val Thr Pro Pro Thr Pro Glu Gly Arg Thr 965 970 975	34165
	CTC GGG GAC CGG GCC GGC GGC CTC GCA CGT CAG GGG GCC ACG GTG Leu Gly Asp Arg Ala Ala Gly Ala Leu Ala Arg Gln Gly Ala Thr Val 980 985 990	34213

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	GAA CGG CTG GTG GTC GAT CCG GTC GCC CTC CGA CGC GAC GGG CTC GCG Glu Arg Leu Val Val Asp Pro Val Ala Val Gly Arg Asp Gly Leu Ala 995 1000 1005 1010	34261
5	GCG CGC CTG GGC GAA CGG TGG GAC GGT GTG CTG TCC CTG CTC GGC GCC Ala Arg Leu Gly Glu Arg Trp Asp Gly Val Leu Ser Leu Leu Gly Ala 1015 1020 1025	34309
10	GAC GAG CGT CCG CTC CCA CGG CAT CCC GCC CTC AAC CGC GCC GTC ATG Asp Glu Arg Pro Leu Pro Arg His Pro Ala Leu Asn Arg Ala Val Met 1030 1035 1040	34357
15	GCC ACC ACG CTG CTC GCC CAG GCT CTG GAC GCA GGA TGC GAG GCG Gly Thr Thr Leu Leu Ala Gln Ala Ala Leu Asp Ala Gly Cys Glu Ala 1045 1050 1055	34405
20	CGG ATA TGG GCC GTG ACG CGG GAG GCC GTC GCC GTC TCC CCG AGC GAG Arg Ile Trp Ala Val Thr Arg Glu Ala Val Ala Val Ser Pro Ser Glu 1060 1065 1070	34453
25	GTG CCG CGG GAC GCC GGC GCG CAG CTC TGG GGG CTC GGG CGG CGC ATC Val Pro Arg Asp Ala Gly Ala Gln Leu Trp Gly Leu Gly Arg Gly Ile 1075 1080 1085 1090	34501
30	GCG CTG GAA CAC CCC TCC CTC TGG GGC GGA TTG ATC GAT CTG CCC GCC Ala Leu Glu His Pro Ser Leu Trp Gly Gly Leu Ile Asp Leu Pro Ala 1095 1100 1105	34549
35	GTG CCG GAC GAA CGC GCG TGG GCC AGG GCC GTC CGG CGG CTC GTC CCG Val Pro Asp Glu Arg Ala Trp Ala Arg Ala Val Arg Arg Leu Val Pro 1110 1115 1120	34597
40	CAC GGT GAG GAC CAG ATC GCC GCG CGC GCC TCG GGT GCC TAT GGG CGC His Gly Glu Asp Gln Ile Ala Ala Arg Ala Ser Gly Ala Tyr Gly Arg 1125 1130 1135	34645
45	AGG CTC CTG CCG GCT CCG CCG GCC GCG TCG CGC CGC ACC TGC ACA CCG Arg Leu Leu Pro Ala Pro Pro Ala Ala Ser Arg Arg Thr Cys Thr Pro 1140 1145 1150	34693
50	TCC GGC ACG GTG CTG GTC ACC GGC GGT ACG GGA GCG CTC GGC GGT CAT Ser Gly Thr Val Leu Val Thr Gly Gly Thr Gly Ala Leu Gly Gly His 1155 1160 1165 1170	34741
55	CTG GCC CGC CGT CTC GCA CGC GGC GGG ACC GGG CAT CTG GTG CTC ACC Leu Ala Arg Arg Leu Ala Arg Gly Gly Thr Gly His Leu Val Leu Thr 1175 1180 1185	34789
	AGC CGT CGC CGC CCG GAC GCG CCG GGC GCC GGT GAA CTC GCC GGT GAA Ser Arg Arg Gly Pro Asp Ala Pro Gly Ala Gly Glu Leu Ala Gly Glu 1190 1195 1200	34837
	CTC GCC TCC CTG GGC GCG AAG GTC ACG GTC GCC GCG TGC GAC ATG GCC Leu Ala Ser Leu Gly Ala Lys Val Thr Val Ala Ala Cys Asp Met Ala 1205 1210 1215	34885
	GAC CGT GAA GCC GTG CGG GCG CTG CTC GAC GAG CAC CGG CCG ACC GCG Asp Arg Glu Ala Val Arg Ala Leu Leu Asp Glu His Arg Pro Thr Ala 1220 1225 1230	34933

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	GTG TTC CAC ACG GCG GGC ACG CCC CAC TCG GCG GAG TTC ACG GCG CTG Val Phe His Thr Ala Gly Thr Pro His Ser Ala Glu Phe Thr Ala Leu 1235 1240 1245 1250	34981
5	GAC GAG ACG ACG ACG GCC GGG GTG TAC GGC GGG AAG GTC CTG GGT GCC Asp Glu Thr Thr Ala Gly Val Tyr Gly Gly Lys Val Leu Gly Ala 1255 1260 1265	35029
10	CGG CAT CTG GAC GAA CTG ACC CGG GAA CTC GGC ATC GGG CTG GAC GCG Arg His Leu Asp Glu Leu Thr Arg Glu Leu Gly Ile Gly Leu Asp Ala 1270 1275 1280	35077
15	TTC GTC CTC TTC TCC TCC GGC GCC GCG GTC TGG GGC AGC GGC GGC CAG Phe Val Leu Phe Ser Ser Gly Ala Ala Val Trp Gly Ser Gly Gly Gln 1285 1290 1295	35125
20	ACC GCT TAC GGG GCC GCG AAC GCC GCG CTG GAC GCC CTC GCC GAG CGG Thr Ala Tyr Gly Ala Ala Asn Ala Ala Leu Asp Ala Leu Ala Glu Arg 1300 1305 1310	35173
25	CGC CGT GCC GCC GGG CTG CCC GCG ACC TCC GTC GCC TGG GGC CTG TGG Arg Arg Ala Ala Gly Leu Pro Ala Thr Ser Val Ala Trp Gly Leu Trp 1315 1320 1325 1330	35221
30	GGC GGC GGA GGC ATG GGG GAG GGG GAC GGT GAG GAG TTC CTC AGC CGG Gly Gly Gly Met Gly Glu Gly Asp Gly Glu Glu Phe Leu Ser Arg 1335 1340 1345	35269
35	CGC GGC CTC GGC GTG ATG CCG CCG GAG GAC GCG CTG GAA GCC CTG GAC Arg Gly Leu Gly Val Met Pro Pro Glu Asp Ala Leu Glu Ala Leu Asp 1350 1355 1360	35317
40	CGG GCC CTG GAC CGG GAG GAC ACC ACC GTC GTG GTG GCG GAT GTC GAC Arg Ala Leu Asp Arg Glu Asp Thr Thr Val Val Val Ala Asp Val Asp 1365 1370 1375	35365
45	TGG GAG CGG TTC GCC CCG GCC TTC ACC GCG TTC CCG CCC AGT GCG CTG Trp Glu Arg Phe Ala Pro Ala Phe Thr Ala Phe Arg Pro Ser Ala Leu 1380 1385 1390	35413
50	ATC TCC CGG CTG GTC TCG GAC GGC GGG GAG GCG GGG GGG CAG GAC GCC Ile Ser Arg Leu Val Ser Asp Gly Gly Glu Ala Gly Gly Gln Asp Ala 1395 1400 1405 1410	35461
55	CCG GAC GGC ACG CTG TTC GCC GCC GGG TTC GCG GGC GCC GGG CCA CTG Pro Asp Gly Thr Leu Phe Ala Ala Gly Phe Ala Ala Ala Gly Pro Leu 1415 1420 1425	35509
	GAG CGG CAG GAG ATG CTG CTC GGC CTG GTG CGC CGG CAT GTG GCC GCC Glu Arg Gln Glu Met Leu Leu Gly Leu Val Arg Arg His Val Ala Ala 1430 1435 1440	35557
	GTA CTC GGC CAC CCG GGG ACC GCG GAC ATC GGT CCC GAC CGT GCT TTC Val Leu Gly His Pro Gly Thr Ala Asp Ile Gly Pro Asp Arg Ala Phe 1445 1450 1455	35605
	AAG GAG CTG GGG TTC AGT TCG GTC ACC GCC GTC GAG CTG GCC GGG CGG Lys Glu Leu Gly Phe Ser Ser Val Thr Ala Val Glu Leu Ala Gly Arg 1460 1465 1470	35653

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	CTG GGC CGG GAG TGC GGA CGG AAG CTG CCG CCG ACG CTG GTC TTC GAC Leu Gly Arg Glu Cys Gly Arg Lys Leu Pro Pro Thr Leu Val Phe Asp 1475 1480 1485 1490	35701
5	CAT CCG ACT GCC GCG GCG GCC GTC GAA CAC CTG GCG GAG CTG CTG ACA His Pro Thr Ala Ala Ala Ala Val Glu His Leu Ala Glu Leu Leu Thr 1495 1500 1505	35749
10	CCG CCC GCC GGT CCC GCC GGT CCC CGG GAG GAG GAG GCG CGG GCC Pro Pro Ala Gly Pro Ala Ala Gly Pro Arg Glu Glu Glu Ala Arg Ala 1510 1515 1520	35797
15	GCC CTG GCG CGC GTG CCG CTC GAA CGG CTG AGG GAA GCC GGC CTG CTG Ala Leu Ala Arg Val Pro Leu Glu Arg Leu Arg Glu Ala Gly Leu Leu 1525 1530 1535	35845
15	GAC GCA CTG CTG CGG CTC GCC GCG GAC GAA TCC GGG GCG ACA ACC CCC Asp Ala Leu Leu Arg Leu Ala Ala Asp Glu Ser Gly Ala Thr Thr Pro 1540 1545 1550	35893
20	CGT ACG TCT GCC GCG TCC GGC GCA CCC CGC GGC CGG GAG GAG CCG GAC Arg Thr Ser Ala Ala Ser Gly Ala Pro Arg Gly Arg Glu Glu Pro Asp 1555 1560 1565 1570	35941
25	GGC CGC GGC GAG CCG GAC GGC TCG GGA CAC CGC GAA AGC CCG GAC GCG Gly Arg Gly Glu Pro Asp Gly Ser Gly His Arg Glu Ser Pro Asp Ala 1575 1580 1585	35989
30	GCC GGC GGG TCG GAC GCC CTG GAC GAT CTC GAC GGG GAC GCC CTG GTG Ala Gly Gly Ser Asp Ala Leu Asp Asp Leu Asp Gly Asp Ala Leu Val 1590 1595 1600	36037
30	CGG CTC GCC CTC GGG GAA CCG GGC GAG TGA CCGGCCGGCG GAGCACACCC Arg Leu Ala Leu Gly Glu Pro Gly Glu * 1605 1610	36087
35	GGCCGTCTCC GGCCCCGGCG CGGCCGGGCC GGAAGCCATC CGCCGCCAAC CCGGTACCGA	36147
40	CCCCCTCAAGC CCTTCAAGCC CTTCGACCCG TCCGATCAGT CAGTCCGGCG GTCCTCCACG ACCGGTCCGG AATCGCCCCC ACACGAGTCA GGAAGCACAC C ATG GCC ATG TCC Met Ala Met Ser 1	36260
45	GCC GAG AGG CTG ACG GAG GCG CTG CGG ACC TCG CTC AAG GAG GCC GAG Ala Glu Arg Leu Thr Glu Ala Leu Arg Thr Ser Leu Lys Glu Ala Glu 5 10 15 20	36308
45	CGG CTC CGG CGG CAG AAC CGC GAA CTG AGG GCC GCG CGG GAC GCG GCG Arg Leu Arg Arg Gln Asn Arg Glu Leu Arg Ala Ala Arg Asp Ala Ala 25 30 35	36356
50	CGG GAG CCG ATC GCC GTC GTC GGC ATG GCC TGC CGC TAC CCG GGC GGT Arg Glu Pro Ile Ala Val Val Gly Met Ala Cys Arg Tyr Pro Gly Gly 40 45 50	36404
55	GTC ACC GGC CCC GAG GAG CTG TGG GAG CTG GTG GCC GGA GGC CGG GAC Val Thr Gly Pro Glu Glu Leu Trp Glu Leu Val Ala Gly Gly Arg Asp 55 60 65	36452

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	GCG ATC GGG CCG TTC CCC GTG GAC CGG CCC TGG GAC GTG GCG TCG CTG Ala Ile Gly Pro Phe Pro Val Asp Arg Gly Trp Asp Val Ala Ser Val 70 75 80	36500
5	TAC GAC CCG GAT CCC GAG TCG AAG GGC ACC ACG TAC TGC CGG GAG GGC Tyr Asp Pro Asp Pro Glu Ser Lys Gly Thr Thr Tyr Cys Arg Glu Gly 85 90 95 100	36548
10	GGG TTC CTG GAA GGC GCC GGT GAC TTC GAC GCC GCC TTC TTC GGC ATC Gly Phe Leu Glu Gly Ala Gly Asp Phe Asp Ala Ala Phe Phe Gly Ile 105 110 115	36596
15	TCG CCG CGC GAG GCC CTG GTG ATG GAC CCG CAG CGG CTG CTG CTG Ser Pro Arg Glu Ala Leu Val Met Asp Pro Gln Gln Arg Leu Leu Leu 120 125 130	36644
20	GAG GTG TCC TGG GAG GCG CTG GAA CGC GCG GGC ATC GAC CCG TCC TCG Glu Val Ser Trp Glu Ala Leu Glu Arg Ala Gly Ile Asp Pro Ser Ser 135 140 145	36692
25	CTG CGC GGC AGC CGC GGT GGT GTC TAC GTG GGC GCC GCG CAC GGC TCG Leu Arg Gly Ser Arg Gly Val Tyr Val Gly Ala Ala His Gly Ser 150 155 160	36740
30	TAC GCC TCC GAT CCC CGG CTG GTG CCC GAG GGC TCG GAG GGC TAT CTG Tyr Ala Ser Asp Pro Arg Leu Val Pro Glu Gly Ser Glu Gly Tyr Leu 165 170 175 180	36788
35	CTG ACC GGC AGC GCC GAC GCG GTG ATG TCC GGC CGC ATC TCC TAC GCG Leu Thr Gly Ser Ala Asp Ala Val Met Ser Gly Arg Ile Ser Tyr Ala 185 190 195	46836
40	CTC GGT CTC GAA GGA CCG TCC ATG ACG GTG GAG ACG GCC TGC TCC TCC Leu Gly Leu Glu Gly Pro Ser Met Thr Val Glu Thr Ala Cys Ser Ser 200 205 210	36884
45	TCG CTG GTG GCG CTG CAT CTG GCG GTA CGG GCG CTG CGG CAC GGC GAG Ser Leu Val Ala Leu His Leu Ala Val Arg Ala Leu Arg His Gly Glu 215 220 225	36932
50	TGC GGG CTC GCG CTG GCG GGC GGG GTG GCG CTG ATG GCC GAT CCG GCG Cys Gly Leu Ala Leu Ala Gly Val Ala Val Met Ala Asp Pro Ala 230 235 240	36980
55	GCG TTC GTG GAG TTC TCC CGG CAG AAG GGG CTG GCC GCC GAC GGC CGC Ala Phe Val Glu Phe Ser Arg Gln Lys Gly Leu Ala Ala Asp Gly Arg 245 250 255 260	37028
	TGC AAG GCG TTC TCG GCC GCC GAC GGC ACC GGC TGG GCC GAG GGC Cys Lys Ala Phe Ser Ala Ala Asp Gly Thr Gly Trp Ala Glu Gly 265 270 275	37076
	GTC GGC GTG CTC GTC CTG GAG CGG CTG TCG GAC GCG CGC CGC GCG GGG Val Gly Val Leu Val Leu Glu Arg Leu Ser Asp Ala Arg Arg Ala Gly 280 285 290	37124
	CAC ACG GTC CTC GGC CTG GTC ACC GGC ACC GCG GTC AAC CAG GAC GGT His Thr Val Leu Gly Leu Val Thr Gly Thr Ala Val Asn Gln Asp Gly 295 300 305	37172

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	GCC TCC AAC GGG CTG ACC GCG CCC AAC GGC CCA GCC CAG CAA CGC GTC Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ala Gln Gln Arg Val 310 315 320	37220
5	ATC GCC GAG GCG CTC GCC GAC GCC GGG CTG TCC CCG GAG GAC GTG GAC Ile Ala Glu Ala Leu Ala Asp Ala Gly Leu Ser Pro Glu Asp Val Asp 325 330 335 340	37268
10	GCG GTC GAG GCG CAC GGC ACC GGC ACC CGG CTC GGC GAC CCC ATC GAG Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu 345 350 355	37316
15	GCC GGG GCG CTG CTC GCC GCC TCC GGA CGG AAC CGT TCC GGC GAC CAC Ala Gly Ala Leu Leu Ala Ala Ser Gly Arg Asn Arg Ser Gly Asp His 360 365 370	37364
20	CCG CTG TGG CTC GGC TCG CTG AAG TCC AAC ATC GGG CAT GCC CAG GCC Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln Ala 375 380 385	37412
25	GCC GCC GGT GTC GGC GGC GTC ATC AAG ATG CTC CAG GCG CTG CGG CAC Ala Ala Gly Val Gly Val Ile Lys Met Leu Gln Ala Leu Arg His 390 395 400	37460
30	GGC TTG CTG CCC CGC ACC CTC CAC GCC GAC GAG CCG ACC CCG CAT GCC Gly Leu Leu Pro Arg Thr Leu His Ala Asp Glu Pro Thr Pro His Ala 405 410 415 420	37508
35	GAC TGG AGC TCC GGC CGG GTA CGG CTG CTC ACC TCC GAG GTG CCG TGG Asp Trp Ser Ser Gly Arg Val Arg Leu Leu Thr Ser Glu Val Pro Trp 425 430 435	37556
40	CAG CGG ACC GGC CGG CCC CGG CGG ACC GGG GTG TCC GCC TTC GGC GTC Gln Arg Thr Gly Arg Pro Arg Arg Thr Gly Val Ser Ala Phe Gly Val 440 445 450	37604
45	GGC GGC ACC AAT GCC CAT GTC GTC CTC GAA GAG GCA CCC GCC CCG CCC Gly Gly Thr Asn Ala His Val Val Leu Glu Glu Ala Pro Ala Pro Pro 455 460 465	37652
50	GCG CCG GAA CCG GCC GGG GAG GCC CCC GGC GGC TCC CGC GCC GCA GAA Ala Pro Glu Pro Ala Gly Glu Ala Pro Gly Gly Ser Arg Ala Ala Glu 470 475 480	37700
55	GGG GCG GAA GGG CCC CTG GCC TGG GTG GTC TCC GGA CGC GAC GAG CCG Gly Ala Glu Gly Pro Leu Ala Trp Val Val Ser Gly Arg Asp Glu Pro 485 490 495 500	37748
55	GCC CTG CGG TCC CAG GCC CGG CGG CTC CGC GAC CAC CTC TCC CGC ACC Ala Leu Arg Ser Gln Ala Arg Arg Leu Arg Asp His Leu Ser Arg Thr 505 510 515	37796
55	CCC GGG GCC CGC CCG CGT GAC ATC GCC TTC TCC CTC GCC GCC ACG CGC Pro Gly Ala Arg Pro Arg Asp Ile Ala Phe Ser Leu Ala Ala Thr Arg 520 525 530	37844
55	GCA GCC TTT GAC CAC CGC GCC GTG CTG ATC GGC TCG GAC GGG GCC GAA Ala Ala Phe Asp His Arg Ala Val Leu Ile Gly Ser Asp Gly Ala Glu 535 540 545	37892

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	CTC GCC GCC GCC CTG GAC GCG TTG GCC GAA GGA CGC GAC GGT CCG GCG Leu Ala Ala Ala Leu Asp Ala Leu Ala Glu Gly Arg Asp Gly Pro Ala 550 555 560	37940
5	GTG GTG CGC GGA GTC CGC GAC CGG GAC GGC AGC ATG GCC TTC CTC TTC Val Val Arg Gly Val Arg Asp Arg Asp Gly Arg Met Ala Phe Leu Phe 565 570 575 580	37988
10	ACC GGG CAG GGC AGC CAG CGC GCC GGG ATG GCC CAC GAC CTG CAT GCC Thr Gly Gln Gly Ser Gln Arg Ala Gly Met Ala His Asp Leu His Ala 585 590 595	38036
15	GCC CAT ACC TTC TTC GCG TCC GCC CTC GAC GAG GTG ACG GAC CGT CTC Ala His Thr Phe Phe Ala Ser Ala Leu Asp Glu Val Thr Asp Arg Leu 600 605 610	38084
20	GAC CCG CTG CTC GGC CGG CCG CTC GGC GCG CTG CTG GAC GCC CGA CCC Asp Pro Leu Leu Gly Arg Pro Leu Gly Ala Leu Leu Asp Ala Arg Pro 615 620 625	38132
25	GGC TCG CCC GAA GCG GCA CTC CTG GAC CGG ACC GAG TAC ACC CAG CCG Gly Ser Pro Glu Ala Ala Leu Leu Asp Arg Thr Glu Tyr Thr Gln Pro 630 635 640	38180
30	GCG CTC TTC GCC GTC GAG GTG GCG CTC CAC CGG CTG CTG GAG CAC TGG Ala Leu Phe Ala Val Glu Val Ala Leu His Arg Leu Leu Glu His Trp 645 650 655 660	38228
35	GGG ATG CGC CCC GAC CTG CTG CTG GGG CAC TCG GTG GGC GAA CTG GCG Gly Met Arg Pro Asp Leu Leu Leu Gly His Ser Val Gly Glu Leu Ala 665 670 675	38276
40	GCC GCC CAC GTC GCG GGT GTG CTC GAT CTC GAC GAC GCC TGC GCG CTG Ala Ala His Val Ala Gly Val Leu Asp Leu Asp Asp Ala Cys Ala Leu 680 685 690	38324
45	GTG GCC GCC CGC GGC AGG CTG ATG CAG CGC CTG CCG CCC GGC GGC GCG Val Ala Ala Arg Gly Arg Leu Met Gln Arg Leu Pro Pro Gly Gly Ala 695 700 705	38372
50	ATG GTC TCC GTG CGG GCC GGC GAG GAC GAG GTC CGC GCA CTG CTG GCC Met Val Ser Val Arg Ala Gly Glu Asp Glu Val Arg Ala Leu Leu Ala 710 715 720	38420
55	GGC CGC GAG GAC GCC GTC GTC GCC GCG GTG AAC GGC CCC CGG TCG Gly Arg Glu Asp Ala Val Cys Val Ala Ala Val Asn Gly Pro Arg Ser 725 730 735 740	38468
	GTG GTG ATC TCC GGC GCG GAG GAA GCG GTG GCC GAG GCG GCG CAG Val Val Ile Ser Gly Ala Glu Glu Ala Val Ala Glu Ala Ala Gln 745 750 755	38516
	CTC GCC GGA CGA CGC CGC ACC AGG CGG CTC CGC GTC GCG CAC GCC Leu Ala Gly Arg Gly Arg Arg Thr Arg Arg Leu Arg Val Ala His Ala 760 765 770	38564
	TTC CAC TCA CCC CTG ATG GAC GGC ATG CTC GCC GGA TTC CCG GAG GTC Phe His Ser Pro Leu Met Asp Gly Met Leu Ala Gly Phe Arg Glu Val 775 780 785	38612

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	GCC GCC GGC CTG CGC TAC CGG GAA CCG GAG CTG ACG GTC GTC TCC ACG Ala Ala Gly Leu Arg Tyr Arg Glu Pro Glu Leu Thr Val Val Ser Thr 790 795 800	38660
5	GTC ACG GGG CGG CCC GCC CGC CCC GGT GAA CTC ACC GGC CCC GAC TAC Val Thr Gly Arg Pro Ala Arg Pro Gly Glu Leu Thr Gly Pro Asp Tyr 805 810 815 820	38708
10	TGG GTG GCC CAG GTC CGT GAG CCC GTG CGC TTC GCG GAC GCG GTC CGC Trp Val Ala Gln Val Arg Glu Pro Val Arg Phe Ala Asp Ala Val Arg 825 830 835	38756
15	ACG GCA CAC CGC CTC GGA GCC CGC ACC TTC CTG GAG ACC GGC CCG GAC Thr Ala His Arg Leu Gly Ala Arg Thr Phe Leu Glu Thr Gly Pro Asp 840 845 850	38804
20	GGC GTG CTG TGC GGC ATG GCA GAG GAG TGC CTG GAG GAC GAC ACC GTG Gly Val Leu Cys Gly Met Ala Glu Glu Cys Leu Glu Asp Asp Thr Val 855 860 865	38852
25	GCC CTG CTG CCG GCG ATC CAC AAG CCC GGC ACC GCG CCG CAC GGT CCG Ala Leu Leu Pro Ala Ile His Lys Pro Gly Thr Ala Pro His Gly Pro 870 875 880	38900
30	GCG GCT CCC GGC GCG CTG CGG GCG GCC GCC GCG TAC GGC CGG GGC Ala Ala Pro Gly Ala Leu Arg Ala Ala Ala Ala Tyr Gly Arg Gly 885 890 895 900	38948
35	GCC CGG GTG GAC TGG GCC GGG ATG CAC GCC GAC GGC CCC GAG GGG CCG Ala Arg Val Asp Trp Ala Gly Met His Ala Asp Gly Pro Glu Gly Pro 905 910 915	38996
40	GCC CGC CGC GTC GAA CTG CCC GTC CAC GCC TTC CGG CAC CGC CGC TAC Ala Arg Arg Val Glu Leu Pro Val His Ala Phe Arg His Arg Arg Tyr 920 925 930	39044
45	TGG CTC GCC CCG GGC CGC GCG GAC ACC GAC GAC TGG ATG TAC CGG Trp Leu Ala Pro Gly Arg Ala Ala Asp Thr Asp Asp Trp Met Tyr Arg 935 940 945	39092
50	ATC GGC TGG GAC CGG CTG CCG GCT GTG ACC GGC GGG GCC CGG ACC GCC Ile Gly Trp Asp Arg Leu Pro Ala Val Thr Gly Gly Ala Arg Thr Ala 950 955 960	39140
55	GGC CGC TGG CTG GTG ATC CAC CCC GAC AGC CCG CGC TGC CGG GAG CTG Gly Arg Trp Leu Val Ile His Pro Asp Ser Pro Arg Cys Arg Glu Leu 965 970 975 980	39188
60	TCC GGC CAC GCC GAA CGC GCG CTG CGC GCC GCG GGC GCG AGC CCC GTA Ser Gly His Ala Glu Arg Ala Leu Arg Ala Ala Gly Ala Ser Pro Val 985 990 995	39236
65	CCG CTG CCC GTG GAC GCT CCG GCC GCC GAC CGG GCG TCC TTC GCG GCA Pro Leu Pro Val Asp Ala Pro Ala Ala Asp Arg Ala Ser Phe Ala Ala 1000 1005 1010	39284
70	CTG CTG CGC TCC GCC ACC GGA CCT GAC ACA CGA GGT GAC ACA GCC GCG Leu Leu Arg Ser Ala Thr Gly Pro Asp Thr Arg Gly Asp Thr Ala Ala 1015 1020 1025	39332

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	CCC GTG GCC GGT GTG CTG TCG CTG CTG TCC GAG GAG GAT CGG CCC CAT Pro Val Ala Gly Val Leu Ser Leu Leu Ser Glu Glu Asp Arg Pro His 1030 1035 1040	39380
5	CGC CAG CAC GCC CCG GTA CCC GCC GGG GTC CTG GCG ACG CTG TCC CTG Arg Gln His Ala Pro Val Pro Ala Gly Val Leu Ala Thr Leu Ser Leu 1045 1050 1055 1060	39428
10	ATG CAG GCT ATG GAG GAG GAG GCG GTG GAG GCT CGC GTG TGG TGC GTC Met Gln Ala Met Glu Glu Ala Val Glu Ala Arg Val Trp Cys Val 1065 1070 1075	39476
15	TCC CGC GCC GCG GTC GCC GCC GAC CGG GAA CGG CCC GTC GGC GCG Ser Arg Ala Ala Val Ala Ala Asp Arg Glu Arg Pro Val Gly Ala 1080 1085 1090	39524
20	GGC GCC GCC CTG TGG GGG CTG GGG CGG GTG GCC GCC CTG GAA CGC CCC Gly Ala Ala Leu Trp Gly Leu Gly Arg Val Ala Ala Leu Glu Arg Pro 1095 1100 1105	39572
25	ACC CGG TGG GGC GGT CTC GTG GAC CTG CCC GCC TCG CCC GGT GCG GCG Thr Arg Trp Gly Gly Leu Val Asp Leu Pro Ala Ser Pro Gly Ala Ala 1110 1115 1120	39620
30	CAC TGG GCG GCC GCC GTG GAA CGG CTC GCC GGT CCC GAG GAC CAG ATC His Trp Ala Ala Ala Val Glu Arg Leu Ala Gly Pro Glu Asp Gln Ile 1125 1130 1135 1140	39668
35	GCC GTG CGC GCG TCC GGC AGT TGG GGC CGG CGC CTC ACC ACC AGG CTG CCG Ala Val Arg Ala Ser Gly Ser Trp Gly Arg Arg Leu Thr Arg Leu Pro 1145 1150 1155	39716
40	CGC GAC GGC GGC CGG ACG GCC GCA CCC GCG TAC CGG CCG CGC GGC Arg Asp Gly Gly Arg Thr Ala Ala Pro Ala Tyr Arg Pro Arg Gly 1160 1165 1170	39764
45	ACG GTG CTC GTC ACC GGT GGC ACC GGC GCG CTC CGC GGG CAT CTC GCC Thr Val Leu Val Thr Gly Gly Thr Gly Ala Leu Gly Gly His Leu Ala 1175 1180 1185	39812
50	CGC TGG CTC GCC GCG GGC GCC GAA CAC CTG GCG CTC ACC ACC CGC Arg Trp Leu Ala Ala Ala Gly Ala Glu His Leu Ala Leu Thr Ser Arg 1190 1195 1200	39860
55	CGG GGC CCG GAC GCG CCC GGC GCC GGA CTC GAG GCC GAA CTC CTC Arg Gly Pro Asp Ala Pro Gly Ala Ala Gly Leu Glu Ala Glu Leu Leu 1205 1210 1215 1220	39908
60	CTC CTG GGC GCC AAG GTG ACG TTC GCC GCC TGC GAC ACC GCC GAC CGC Leu Leu Gly Ala Lys Val Thr Phe Ala Ala Cys Asp Thr Ala Asp Arg 1225 1230 1235	39956
65	GAC GGC CTC GCC CGG GTC CTG CGG GCG ATA CCG GAG GAC ACC CCG CTC Asp Gly Leu Ala Arg Val Leu Arg Ala Ile Pro Glu Asp Thr Pro Leu 1240 1245 1250	40004
70	ACC GCG GTG TTC CAC GCC GCG GGC GTA CCG CAG GTC ACG CCG CTG TCC Thr Ala Val Phe His Ala Ala Gly Val Pro Gln Val Thr Pro Leu Ser 1255 1260 1265	40052

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	CGT ACC TCG CCC GAG CAC TTC GCC GAC CTG TAC GCG CCC AAG GCG GCG Arg Thr Ser Pro Glu His Phe Ala Asp Val Tyr Ala Gly Lys Ala Ala 1270 1275 1280	40100
5	GGA GCC GCG CAC CTG GAC GAA CTG ACC CGC GAA CTC GGC GCC GGA CTC Gly Ala Ala His Leu Asp Glu Leu Thr Arg Glu Leu Gly Ala Gly Leu 1285 1290 1295 1300	40148
10	GAC GCG TTC GTC CTC TAC TCC TCC GGC GCC GGC GTC TGG GGC AGC GCC Asp Ala Phe Val Leu Tyr Ser Ser Gly Ala Gly Val Trp Gly Ser Ala 1305 1310 1315	40196
15	GGA CAG GGT GCC TAC GCC GCC AAC GCC GGC CTG GAC GCG CTC GCC Gly Gln Gly Ala Tyr Ala Ala Ala Asn Ala Ala Leu Asp Ala Leu Ala 1320 1325 1330	40244
20	CGG CGC CGT GCG GCG GAC GGA CTC CCC GCC ACC TCC ATC GCC TGG GGC Arg Arg Arg Ala Ala Asp Gly Leu Pro Ala Thr Ser Ile Ala Trp Gly 1335 1340 1345	40292
25	GTG TGG GGC GGC GGC GGT ATG GGG GCC GAC GAG GCG GGC GCG GAG TAT Val Trp Gly Gly Met Gly Ala Asp Glu Ala Gly Ala Glu Tyr 1350 1355 1360	40340
30	CTG GGC CGG CGC GGT ATG CGC CCC ATG GCA CCG GTC TCC GCG CTC CGG Leu Gly Arg Arg Gly Met Arg Pro Met Ala Pro Val Ser Ala Leu Arg 1365 1370 1375 1380	40388
35	GCG ATG GCC ACC GCC ATC GCC TCC GGG GAA CCC TGC CCC ACC GTC ACC Ala Met Ala Thr Ala Ile Ala Ser Gly Glu Pro Cys Pro Thr Val Thr 1385 1390 1395	40436
40	CAC ACC GAC TGG GAG CGC TTC GGC GAG GGC TTC ACC GCC TTC CGG CCC His Thr Asp Trp Glu Arg Phe Gly Glu Gly Phe Thr Ala Phe Arg Pro 1400 1405 1410	40484
45	AGC CCT CTG ATC GCG GGG CTC GGC ACG CCG GGC GGC CGG CGG GCG GCG Ser Pro Leu Ile Ala Gly Leu Gly Thr Pro Gly Gly Arg Ala Ala 1415 1420 1425	40532
50	GAG ACC CCC GAG GAG GGG AAC GCC ACC GCT GCG GCG GAC CTC ACC GCC Glu Thr Pro Glu Glu Gly Asn Ala Thr Ala Ala Ala Asp Leu Thr Ala 1430 1435 1440	40580
55	CTG CCG CCC GCC GAA CTC CGC ACC GCG CTG CGC GAG CTG GTG CGA GCC Leu Pro Pro Ala Glu Leu Arg Thr Ala Leu Arg Glu Leu Val Arg Ala 1445 1450 1455 1460	40628
	CGG ACC GCC GCG GCG CTC GGC CTC GAC GAT CCG GCC GAG GTC GCC GAG Arg Thr Ala Ala Leu Gly Leu Asp Asp Pro Ala Glu Val Ala Glu 1465 1470 1475	40676
	GGC GAA CGG TTC CCC GCC ATG GGC TTC GAC TCC CTG GCC ACC GTA CGG Gly Glu Arg Phe Pro Ala Met Gly Phe Asp Ser Leu Ala Thr Val Arg 1480 1485 1490	40724
	CTG CGC CGC GGA CTC GCC TCG GCC ACG GGC CTC GAC CTG CCC CCC GAT Leu Arg Arg Gly Leu Ala Ser Ala Thr Gly Leu Asp Leu Pro Pro Asp 1495 1500 1505	40772

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	CTG CTC TTC GAC CGG GAC ACC CCG GCC GCG CTC CCC CAC CTG GCC Leu Leu Phe Asp Arg Asp Thr Pro Ala Ala Leu Ala Ala His Leu Ala 1510 1515 1520	40820
5	GAA CTG CTC GCC ACC GCA CGG GAC CAC GGA CCC GGC GGC CCC GGG ACC Glu Leu Leu Ala Thr Ala Arg Asp His Gly Pro Gly Gly Pro Gly Thr 1525 1530 1535 1540	40868
10	GGT GCC GCG CCG GCC GAT GCC GGA AGC GGC CTG CCG GCC CTC TAC CGG Gly Ala Ala Pro Ala Asp Ala Gly Ser Gly Leu Pro Ala Leu Tyr Arg 1545 1550 1555	40916
15	GAG GCC GTC CGC ACC GGC CGG GCC GCG GAA ATG GCC GAA CTG CTC GCC Glu Ala Val Arg Thr Gly Arg Ala Ala Glu Met Ala Glu Leu Leu Ala 1560 1565 1570	40964
20	GCC GCT TCC CGG TTC CGC CCC GCC TTC GGG ACG GCG GAC CGG CAG CCG Ala Ala Ser Arg Phe Arg Pro Ala Phe Gly Thr Ala Asp Arg Gln Pro 1575 1580 1585	41012
25	GTG GCC CTC GTG CCG CTG GCC GAC GGC GCG GAG GAC ACC GGG CTC CCG Val Ala Leu Val Pro Leu Ala Asp Gly Ala Glu Asp Thr Gly Leu Pro 1590 1595 1600	41060
30	CTG CTC GTG GGC TGC GCC GGG ACG GCG GTG GCC TCC GGC CCG GTG GAG Leu Leu Val Gly Cys Ala Gly Thr Ala Val Ala Ser Gly Pro Val Glu 1605 1610 1615 1620	41108
35	TTC ACC GCC TTC GCC GGA GCG CTG GCG GAC CTC CCG GCG GCG GCC CCG Phe Thr Ala Phe Ala Gly Ala Leu Ala Asp Leu Pro Ala Ala Ala Pro 1625 1630 1635	41156
40	ATG GCC GCG CTG CCG CAG CCC GCC TTT CTG CCG GGA GAA CGA GTC CCG Met Ala Ala Leu Pro Gln Pro Gly Phe Leu Pro Gly Glu Arg Val Pro 1640 1645 1650	41204
45	GCC ACC CCG GAG GCA TTG TTC GAG GCC CAG GCG GAA GCG CTG CTG CGC Ala Thr Pro Glu Ala Leu Phe Glu Ala Gln Ala Glu Ala Leu Leu Arg 1655 1660 1665	41252
50	TAC GCG GCC GGC CGG CCC TTC GTC CTG CTG GGG CAC TCC GCC GGC GGC Tyr Ala Ala Gly Arg Pro Phe Val Leu Leu Gly His Ser Ala Gly Ala 1670 1675 1680	41300
55	AAC ATG GCC CAC GCC CTG ACC CGT CAT CTG GAG GCG AAC GGT GGC GGC Asn Met Ala His Ala Leu Thr Arg His Leu Glu Ala Asn Gly Gly 1685 1690 1695 1700	41348
	CCC GCA GGG CTG GTG CTC ATG GAC ATC TAC ACC CCC GCC GAC CCC GGC Pro Ala Gly Leu Val Leu Met Asp Ile Tyr Thr Pro Ala Asp Pro Gly 1705 1710 1715	41396
	GCG ATG GGC GTC TGG CGG AAC GAC ATG TTC CAG TGG GTC TGG CGG CGC Ala Met Gly Val Trp Arg Asn Asp Met Phe Gln Trp Val Trp Arg Arg 1720 1725 1730	41444
	TCG GAC ATC CCC CCG GAC CAC CGC CTC ACG GCC ATG GGC GCC TAC Ser Asp Ile Pro Pro Asp Asp His Arg Leu Thr Ala Met Gly Ala Tyr 1735 1740 1745	41492

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	CAC CGG CTG CTT CTC GAC TGG TCG CCC ACC CCC GTC CGC GCC CCC GTA His Arg Leu Leu Leu Asp Trp Ser Pro Thr Pro Val Arg Ala Pro Val 1750 1755 1760	41540
5	CTG CAT CTG CGC GCC GCG GAA CCC ATG GGC GAC TGG CCA CCC GGG GAC Leu His Leu Arg Ala Ala Glu Pro Met Gly Asp Trp Pro Pro Gly Asp 1765 1770 1775 1780	41588
10	ACC GGC TGG CAG TCC CAC TGG GAC GGC GCG CAC ACC ACC GCC GGC ATC Thr Gly Trp Gln Ser His Trp Asp Gly Ala His Thr Thr Ala Gly Ile 1785 1790 1795	41636
15	CCC GGA AAC CAC TTC ACG ATG ATG ACC GAA CAC GCC TCC GCC GCC GCC Pro Gly Asn His Phe Thr Met Met Thr Glu His Ala Ser Ala Ala Ala 1800 1805 1810	41684
20	CGG CTC GTG CAC GGC TGG CTC GCG GAA CGG ACC CCG TCC GGG CAG GGC Arg Leu Val His Gly Trp Leu Ala Glu Arg Thr Pro Ser Gly Gln Gly 1815 1820 1825	41732
25	GGG TCA CCG TCC CGC GCG GCG GGG AGA GAG GAG AGG CCG TGA Gly Ser Pro Ser Arg Ala Ala Gly Arg Glu Glu Arg Pro *1830 1835 1840	41774
30	ACACGGCAGC CGGCCCGACC GGCACCGCCG CCGGCGGCAC CACCGCCCCG GCGGCGGCAC	41834
35	ACGACCTGTC CGCGCCCGGA CGCAGGCTCC AACTCACCCG GGCGCACAG TGGTTGCCG GCAACCAGGG AGACCCCTAC GGGATGATCC TGCGCGCCGG CACCGCCGAC CCGGCACCGT ACGAGGAAGA GATCCGTGAG CGGGGGCCGC TGTTCCACAG CGAACTCCTC GGCGCCCTGGG TGACCGGCAG CGGCCATGTC GCCGACGCCG TGACGGCCGA CGACGGCTTC GGCGCCCTCA CCGGGGACGG TGCACGGCCA CGAGTCCCGCG AACTGCCGCT CTCCGGCAGC GCCCTCGACG CCGCCCACGG GAACCCCGGC GGCCCGCCCC TCCCCGGAGG GTGGCCGCAC CGGCCCCCGG ACAGGGAGGA CGAGACGAC CGGGACCGGC ACCGGGGCGGA CCTGCTGAAC GCCGCCGGCC CGGGGCAGGT CCTCGACCTC GTCCCCCTCG CCCGGCGGCT GGCGGCCCGG ACGGCCGGCG 40 CGTGGCTGGG CGTCCCCGGCG GAACGGCTGC CGCGCTTCGA GACGGCACTC ACCGGCTGCC GCCGGGCCCT CGACGCCCTG CTCTGCCCCC AGCTCCTGGC CGACGGCGGG GCCGGACTGG CCGCGGAGGA GGCCCTGCAGC GCCGTGCTCG GCGAGACCCC GGAGGCACCC GGACGTCCGC 45 CCGGGCGGGT CGAGGGCGGCC CGCGGCCACG CCGTCAGCGC GGCGGAGCCC ATCGCCGTCC TGCTGTCAA CGCGGTGCGG GAACTGATGG AACGGCCGGC CCAGTGGCGG GCGCTCACCG CCGACCCCGG CCTGGCGGGC GCCGCGATCA CCGAACACCT GCTCTGGCA CCGCCGGTGC 50 GCCTGGAGAG CAGGGTGGCA CGCGAGACGG CCGTACTCGC CGGGCGGACG CTGCCCCGTG GAACCCATCT CGTCGTCTC GCCGCCGCCG CCAACCGCGA CGGCTGCCGG AACGCCGGTC 55 CGGCCGTAC CGGCTTCGAC GTCCCTCGCC GCGCCTCGGA CGGCGGCCCG CAGCCCCACG	42314
		42374
		42434
		42494
		42554
		42614
		42674
		42734
		42794
		42854

	GACTCCCCGA GGACCTGCAC TTCCGTCCTCT CGGGCCCGCT CGTCCGGCGG ACCGCCGAGG	42914
	CCGGTCTGAG GGCGCTCGCC GAACGCTTCC CCGGCTGCGC CCGGCCGGCC CGCAGTCCG	42974
5	AGTCCGCCGG TCACCGGTGC TCCGGGTCT CGGGCCGGCTG CCCGTCGCCCG CGTATGTCCC	43034
	CGAGTGAGAA GGGCACTGGA TGACCGCCGC CGAGGACCGC ACGGACCGA AGGGAAACCG	43094
	CCGATGCCCG TACTGCTGAC CTGTATCGCG CACAACACCC ACTACTACAA CCTGGTGCCG	43154
10	GTCGCCTGGG CCCTGAGAGC GGCGGACAC GAGGTGCCGG TGGCCGCGCA GCCCGCCCTC	43214
	ACCGACACGA TCACCGCCTC CGGACTGACC GCCGTGCCGG TCGGCGCAA CGAGTCCGTG	43274
15	CTCGAG	43280

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4473 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ser Ala Leu Arg Arg Ala Val Gln Ser Asn Cys Gly Tyr Gly			
1	5	10	15
Asp Leu Met Thr Ser Asn Thr Ala Ala Gln Asn Thr Gly Asp Gln Glu			
20	25	30	
Asp Val Asp Gly Pro Asp Ser Thr His Gly Gly Glu Ile Ala Val Val			
35	40	45	
Gly Met Ser Cys Arg Leu Pro Gly Ala Ala Gly Val Glu Glu Phe Trp			
50	55	60	
Glu Leu Leu Arg Ser Gly Arg Gly Met Pro Thr Arg Gln Asp Asp Gly			
65	70	75	80
Thr Trp Arg Ala Ala Leu Glu Asp His Ala Gly Phe Asp Ala Gly Phe			
85	90	95	
Phe Gly Met Asn Ala Arg Gln Ala Ala Ala Thr Asp Pro Gln His Arg			
100	105	110	
Leu Met Leu Glu Leu Gly Trp Glu Ala Leu Glu Asp Ala Gly Ile Val			
115	120	125	
Pro Gly Asp Leu Thr Gly Thr Asp Thr Gly Val Phe Ala Gly Val Ala			
130	135	140	
Ser Asp Asp Tyr Ala Val Leu Thr Arg Arg Ser Ala Val Ser Ala Gly			
145	150	155	160
Gly Tyr Thr Ala Thr Gly Leu His Arg Ala Leu Ala Ala Asn Arg Leu			
165	170	175	

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Ser His Phe Leu Gly Leu Arg Gly Pro Ser Leu Val Val Asp Ser Ala
 180 185 190
 Gln Ser Ala Ser Leu Val Ala Val Gln Leu Ala Cys Glu Ser Leu Arg
 5 195 200 205
 Arg Gly Glu Thr Ser Leu Ala Val Ala Gly Gly Val Asn Leu Ile Leu
 210 215 220
 Thr Glu Glu Ser Thr Thr Val Met Glu Arg Met Gly Ala Leu Ser Pro
 10 225 230 235 240
 Asp Gly Arg Cys His Thr Phe Asp Ala Arg Ala Asn Gly Tyr Val Arg
 245 250 255
 Gly Glu Gly Gly Ala Val Val Leu Lys Pro Leu Asp Ala Ala Leu
 15 260 265 270
 Ala Asp Gly Asp Arg Val Tyr Cys Val Ile Lys Gly Gly Ala Val Asn
 275 280 285
 20 Asn Asp Gly Gly Ala Ser Leu Thr Thr Pro Asp Arg Glu Ala Gln
 290 295 300
 Glu Ala Val Leu Arg Gln Ala Tyr Arg Arg Ala Gly Val Ser Thr Gly
 25 305 310 315 320
 Ala Val Arg Tyr Val Glu Leu His Gly Thr Gly Thr Arg Ala Gly Asp
 325 330 335
 Pro Val Glu Ala Ala Leu Gly Ala Val Leu Gly Ala Gly Ala Asp
 30 340 345 350
 Ser Gly Arg Ser Thr Pro Leu Ala Val Gly Ser Val Lys Thr Asn Val
 355 360 365
 Gly His Leu Glu Gly Ala Ala Gly Ile Val Gly Leu Ile Lys Ala Thr
 370 375 380
 Leu Cys Val Arg Lys Gly Glu Leu Val Pro Ser Leu Asn Phe Ser Thr
 385 390 395 400
 Pro Asn Pro Asp Ile Pro Leu Asp Asp Leu Arg Leu Arg Val Gln Thr
 40 405 410 415
 Glu Arg Gln Glu Trp Asn Glu Glu Asp Asp Arg Pro Arg Val Ala Gly
 420 425 430
 45 Val Ser Ser Phe Gly Met Gly Gly Thr Asn Val His Leu Val Ile Ala
 435 440 445
 Glu Ala Pro Ala Ala Gly Ser Ser Gly Ala Gly Gly Ser Gly Ala
 50 450 455 460
 Gly Ser Gly Ala Gly Ile Ser Ala Val Ser Gly Val Val Pro Val Val
 465 470 475 480
 Val Ser Gly Arg Ser Arg Val Val Val Arg Glu Ala Ala Gly Arg Leu
 55 485 490 495

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Ala Glu Val Val Glu Ala Gly Gly Val Gly Leu Ala Asp Val Ala Val
 500 505 510

5 Thr Met Ala Asp Arg Ser Arg Phe Gly Tyr Arg Ala Val Val Leu Ala
 515 520 525

Arg Gly Glu Ala Glu Leu Ala Gly Arg Leu Arg Ala Leu Ala Gly Gly
 530 535 540

10 Asp Pro Asp Ala Gly Val Val Thr Gly Ala Val Leu Asp Gly Gly Val
 545 550 555 560

Val Val Gly Ala Ala Pro Gly Gly Ala Gly Ala Ala Gly Gly Ala Gly
 565 570 575

15 Ala Ala Gly Gly Ala Gly Gly Gly Val Val Leu Val Phe Pro Gly
 580 585 590

Gln Gly Thr Gln Trp Val Gly Met Gly Ala Gly Leu Leu Gly Ser Ser
 595 600 605

20 Glu Val Phe Ala Ala Ser Met Arg Glu Cys Ala Arg Ala Leu Ser Val
 610 615 620

His Val Gly Trp Asp Leu Leu Glu Val Val Ser Gly Gly Ala Gly Leu
 625 630 635 640

25 Glu Arg Val Asp Val Val Gln Pro Val Thr Trp Ala Val Met Val Ser
 645 650 655

Leu Ala Arg Tyr Trp Gln Ala Met Gly Val Asp Val Ala Ala Val Val
 30 660 665 670

Gly His Ser Gln Gly Glu Ile Ala Ala Ala Thr Val Ala Gly Ala Leu
 675 680 685

35 Ser Leu Glu Asp Ala Ala Ala Val Val Ala Leu Arg Ala Gly Leu Ile
 690 695 700

Gly Arg Tyr Leu Ala Gly Arg Gly Ala Met Ala Ala Val Pro Leu Pro
 705 710 715 720

40 Ala Gly Glu Val Glu Ala Gly Leu Ala Lys Trp Pro Gly Val Glu Val
 725 730 735

Ala Ala Val Asn Gly Pro Ala Ser Thr Val Val Ser Gly Asp Arg Arg
 740 745 750

45 Ala Val Ala Gly Tyr Val Ala Val Cys Gln Ala Glu Gly Val Gln Ala
 755 760 765

Arg Leu Ile Pro Val Asp Tyr Ala Ser His Ser Arg His Val Glu Asp
 770 775 780

50 Leu Lys Gly Glu Leu Glu Arg Val Leu Ser Gly Ile Arg Pro Arg Ser
 785 790 795 800

Pro Arg Val Pro Val Cys Ser Thr Val Ala Gly Glu Gln Pro Gly Glu
 805 810 815

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Pro Val Phe Asp Ala Gly Tyr Trp Phe Arg Asn Leu Arg Asn Arg Val
 820 825 830
 Glu Phe Ser Ala Val Val Gly Gly Leu Leu Glu Glu Gly His Arg Arg
 5 835 840 845
 Phe Ile Glu Val Ser Ala His Pro Val Leu Val His Ala Ile Glu Gln
 850 855 860
 Thr Ala Glu Ala Ala Asp Arg Ser Val His Ala Thr Gly Thr Leu Arg
 10 865 870 875 880
 Arg Gln Asp Asp Ser Pro His Arg Leu Leu Thr Ser Thr Ala Glu Ala
 885 890 895
 Trp Ala His Gly Ala Thr Leu Thr Trp Asp Pro Ala Leu Pro Pro Gly
 15 900 905 910
 His Leu Thr Thr Leu Pro Thr Tyr Pro Phe Asn His His His Tyr Trp
 915 920 925
 20 Leu Asp Thr Ile Asp Gly Gly Gly Asp Asp Ala Thr Gln Glu Lys
 930 935 940
 Glu Ser Gly Pro Leu Thr Arg Glu Leu Arg Gly Leu Pro Ser Ser Gln
 25 945 950 955 960
 Lys Gln Leu Gly Phe Leu Leu Asp Leu Val Cys Arg His Thr Ala Val
 965 970 975
 Val Leu Gly Leu Asp Thr Ala Ala Glu Val Asp Pro Asp Leu Ser Phe
 30 980 985 990
 Lys Lys Gln Gly Ile Gln Ser Met Thr Gly Val Glu Leu Arg Asn Arg
 995 1000 1005
 Leu Leu Thr Glu Thr Gly Leu Ala Leu Pro Thr Thr Leu Val Tyr Asp
 35 1010 1015 1020
 Arg Pro Thr Pro Arg Ala Leu Ala Gln Phe Leu His Thr Glu Leu Leu
 1025 1030 1035 1040
 Asp Gly Ser Pro Ser Gly Ser Val Leu Ala Pro Ala Gln Lys Ser Phe
 40 1045 1050 1055
 Glu Ala Gln Glu Pro Ile Ala Val Val Gly Met Gly Cys Arg Phe Pro
 1060 1065 1070
 45 Gly Gly Val Gly Ser Pro Glu Ala Leu Trp Arg Leu Val Val Glu Gly
 1075 1080 1085
 Val Asp Ala Val Ser Pro Phe Pro Gly Asp Arg Gly Trp Asp Val Glu
 1090 1095 1100
 50 Gly Leu Tyr Asp Pro Glu Pro Gly Val Ala Gly Lys Ser Tyr Val Arg
 1105 1110 1115 1120
 Glu Gly Gly Phe Leu His Asp Ala Ala Glu Phe Asp Ala Glu Phe Phe
 55 1125 1130 1135

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Gly Ile Ser Pro Arg Glu Ala Val Ala Met Asp Pro Gln Gln Arg Leu
 1140 1145 1150
 5 Leu Leu Glu Thr Ser Trp Glu Ala Ile Glu Arg Ala Gly Ile Asp Pro
 1155 1160 1165
 His Ser Leu His Gly Ser Arg Thr Gly Val Tyr Ala Gly Val Met Pro
 1170 1175 1180
 10 Gln Glu Tyr Gly Pro Arg Leu Ala Glu Gly Ala Glu Gly Ser Asp Gly
 1185 1190 1195 1200
 Tyr Leu Leu Thr Gly Thr Ser Gly Ser Val Val Ser Gly Arg Val Ala
 1205 1210 1215
 15 Tyr Thr Leu Gly Leu Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys
 1220 1225 1230
 Ser Ser Ser Leu Val Ala Leu His Leu Ala Val Gln Ala Leu Arg Gly
 1235 1240 1245
 20 Gly Glu Cys Asp Met Ala Leu Ala Gly Gly Val Thr Val Met Ala Gly
 1250 1255 1260
 25 Pro Gly Met Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Ala Asp
 1265 1270 1275 1280
 Gly Arg Cys Lys Ala Phe Ala Asp Gly Ala Asp Gly Thr Ala Trp Ala
 1285 1290 1295
 Glu Gly Ala Gly Val Val Leu Val Glu Arg Leu Ser Asp Ala Arg Arg
 30 1300 1305 1310
 Leu Gly His Pro Val Leu Ala Val Val Cys Gly Ser Ala Val Asn Gln
 1315 1320 1325
 35 Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ser Gln Glu
 1330 1335 1340
 Arg Val Ile Arg Gln Ala Leu Gly Asn Ala Arg Leu Thr Val Ala Asp
 1345 1350 1355 1360
 40 Val Asp Val Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp Pro
 1365 1370 1375
 Ile Glu Ala Gln Ala Leu Leu Gly Thr Tyr Gly Arg Asp Arg Asp Gly
 1380 1385 1390
 45 Gly Arg Pro Val Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala
 1395 1400 1405
 Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Met
 50 1410 1415 1420
 Arg Tyr Gly Trp Leu Pro Arg Thr Leu His Val Asp Glu Pro Ser Arg
 1425 1430 1435 1440
 His Val Asp Trp Ser Ala Gly Gly Val Trp Leu Leu Thr Glu Ala Arg
 55 1445 1450 1455

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Glu Trp Pro Gly Val Asp Arg Pro Arg Arg Ala Ala Val Ser Ala Phe
 1460 1465 1470
 Gly Val Ser Gly Thr Asn Ala His Leu Ile Leu Glu Ala Pro Asp Thr
 5 1475 1480 1485
 Ala Glu Ala Glu Ser Ala Thr Thr Pro Val Arg Ser Glu Val Ser Glu
 1490 1495 1500
 Ser Ala Ala Val Leu Asp Ala Arg Ser Gly Val Val Pro Val Val Val
 10 1505 1510 1515 1520
 Ser Gly Arg Ser Arg Val Val Val Arg Glu Ala Ala Gly Arg Leu Ala
 1525 1530 1535
 Glu Val Val Glu Ala Gly Gly Val Gly Leu Ala Asp Val Ala Val Thr
 15 1540 1545 1550
 Met Ala Gly Arg Ser Arg Phe Gly Tyr Arg Ala Val Val Leu Ala Arg
 1555 1560 1565
 Gly Glu Ala Glu Leu Ala Gly Arg Leu Arg Ala Leu Ala Gly Gly Asp
 20 1570 1575 1580
 Pro Asp Ala Gly Val Val Thr Gly Ala Val Val Asp Pro Glu Thr Gly
 1585 1590 1595 1600
 Ser Gly Gly Gly Val Val Leu Val Phe Pro Gly Gln Gly Thr Gln
 25 1605 1610 1615
 Trp Val Gly Met Gly Ala Gly Leu Leu Gly Ser Ser Glu Val Phe Ala
 30 1620 1625 1630
 Ala Ser Met Arg Glu Cys Ala Arg Ala Leu Ser Val His Val Glu Trp
 1635 1640 1645
 Asp Leu Leu Glu Val Val Ser Gly Gly Ala Gly Leu Glu Arg Val Asp
 35 1650 1655 1660
 Val Val Gln Pro Val Thr Trp Ala Val Met Val Ser Leu Ala Arg Tyr
 1665 1670 1675 1680
 Trp Gln Ala Met Gly Val Asp Val Ala Ala Val Val Gly His Ser Gln
 40 1685 1690 1695
 Gly Glu Ile Ala Ala Ala Thr Val Ala Gly Ala Leu Ser Leu Glu Asp
 1700 1705 1710
 Ala Ala Ala Val Val Ala Leu Arg Ala Gly Leu Ile Gly Arg Tyr Leu
 45 1715 1720 1725
 Ala Gly Arg Gly Ala Met Ala Ala Val Pro Leu Pro Ala Gly Glu Val
 1730 1735 1740
 Glu Ala Gly Leu Ala Lys Trp Pro Gly Val Glu Val Ala Ala Val Asn
 50 1745 1750 1755 1760
 Gly Pro Ala Ser Thr Val Val Ser Gly Asp Arg Arg Ala Val Ala Gly
 55 1765 1770 1775

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Tyr Val Ala Val Cys Gln Ala Glu Gly Val Gln Ala Arg Leu Ile Pro
 1780 1785 1790
 Val Asp Tyr Ala Ser His Ser Arg His Val Glu Asp Leu Lys Gly Glu
 5 1795 1800 1805
 Leu Glu Arg Val Leu Ser Gly Ile Arg Pro Arg Ser Pro Arg Val Pro
 1810 1815 1820
 Val Cys Ser Thr Val Ala Gly Glu Gln Pro Gly Glu Pro Val Phe Asp
 10 1825 1830 1835 1840
 Ala Gly Tyr Trp Phe Arg Asn Leu Arg Asn Arg Val Glu Phe Ser Ala
 1845 1850 1855
 Val Val Gly Gly Leu Leu Glu Glu Gly His Arg Arg Phe Ile Glu Val
 15 1860 1865 1870
 Ser Ala His Pro Val Leu Val His Ala Ile Glu Gln Thr Ala Glu Ala
 1875 1880 1885
 Ala Asp Arg Ser Val His Ala Thr Gly Thr Leu Arg Arg Gln Asp Asp
 20 1890 1895 1900
 Ser Pro His Arg Leu Leu Thr Ser Thr Ala Glu Ala Trp Ala His Gly
 1905 1910 1915 1920
 Ala Thr Leu Thr Trp Asp Pro Ala Leu Pro Pro Gly His Leu Thr Thr
 25 1925 1930 1935
 Leu Pro Thr Tyr Pro Phe Asn His His Tyr Trp Leu Asp Thr Thr
 30 1940 1945 1950
 Pro Thr Thr Pro Ala Thr Thr Thr Gln Ser Pro Thr Asp Ala Trp Arg
 1955 1960 1965
 Tyr Arg Val Thr Trp Lys Ala Leu Thr Glu Ser Ser Pro Val Arg Pro
 35 1970 1975 1980
 His Ser Ile Gly Arg Cys Leu Leu Val Ala Pro Pro Thr Thr Asp Gly
 1985 1990 1995 2000
 Glu Leu Leu Asp Gly Leu Thr Thr Val Leu Ser Glu Arg Gly Ala Ser
 40 2005 2010 2015
 Val Ala Arg Leu Glu Val Pro Ile Gly Ala Arg Arg Ala Glu Val Ala
 2020 2025 2030
 Glu Leu Leu Lys Pro Ser Met Glu Ser Ala Gly Glu Asn Thr Thr
 45 2035 2040 2045
 Val Val Ser Leu Leu Gly Leu Val Pro Ser Thr Asp Ala Val Arg Thr
 2050 2055 2060
 Ser Ile Ala Leu Leu Gln Ala Val Ser Asp Ile Gly Val Pro Ala Ala
 50 2065 2070 2075 2080
 Arg Val Trp Ala Leu Thr Arg Arg Ala Val Ala Val Val Pro Gly Glu
 55 2085 2090 2095

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Thr Pro Gln Asp Ala Gly Ala Gln Leu Trp Gly Phe Gly Arg Val Ala
 2100 2105 2110
 Ala Leu Glu Leu Pro Asp Ile Trp Gly Gly Leu Ile Asp Leu Pro Glu
 5 2115 2120 2125
 Thr Ala Glu Leu Thr Arg Thr Pro Glu Thr Ser Gln Pro Pro Gln Thr
 2130 2135 2140
 Pro Glu Arg Leu Pro Gln Thr Pro Asn Arg Arg Ala Leu Glu Leu Ala
 10 2145 2150 2155 2160
 Ala Ala Val Leu Ala Gly Arg Asp Gly Glu Asp Gln Val Ala Val Arg
 2165 2170 2175
 Ala Ser Gly Ile Tyr Gly Arg Arg Val Ser Arg Ala Ala Ala Gly
 15 2180 2185 2190
 Ala Ala Ser Trp Gln Pro Ser Gly Thr Val Leu Ile Thr Gly Gly Met
 2195 2200 2205
 20 Gly Ala Ile Gly Arg Arg Leu Ala Arg Arg Leu Ala Ala Glu Gly Ala
 2210 2215 2220
 Glu Arg Leu Val Leu Thr Ser Arg Arg Gly Pro Glu Ala Pro Gly Ala
 2225 2230 2235 2240
 25 Ala Glu Leu Ala Glu Glu Leu Arg Gly His Gly Cys Glu Val Val His
 2245 2250 2255
 Ala Ala Cys Asp Val Ala Glu Arg Asp Ala Leu Ala Ala Leu Val Thr
 30 2260 2265 2270
 Ala Tyr Pro Pro Asn Ala Val Phe His Thr Ala Gly Ile Leu Asp Asp
 2275 2280 2285
 Ala Val Ile Asp Thr Leu Ser Pro Glu Ser Phe Glu Thr Val Arg Gly
 35 2290 2295 2300
 Ala Lys Val Cys Gly Ala Glu Leu Leu His Gln Leu Thr Ala Asp Ile
 2305 2310 2315 2320
 40 Lys Gly Leu Asp Ala Phe Val Leu Phe Ser Ser Val Thr Gly Thr Trp
 2325 2330 2335
 Gly Asn Ala Gly Gln Gly Ala Tyr Ala Ala Ala Asn Ala Ala Leu Asp
 2340 2345 2350
 45 Ala Leu Ala Glu Arg Arg Ala Ala Gly Leu Pro Ala Thr Ser Val
 2355 2360 2365
 Ala Trp Gly Leu Trp Gly Gly Gly Met Ala Ala Gly Ala Gly Glu
 50 2370 2375 2380
 Glu Ser Leu Ser Arg Arg Gly Leu Arg Ala Met Asp Pro Asp Ala Ala
 2385 2390 2395 2400
 Val Asp Ala Leu Leu Gly Ala Met Gly Arg Asn Asp Val Cys Val Thr
 55 2405 2410 2415

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Val Val Asp Val Asp Trp Glu Arg Phe Ala Pro Ala Thr Asn Ala Ile
 2420 2425 2430
 5 Arg Pro Gly Arg Leu Phe Asp Thr Val Pro Glu Ala Arg Glu Ala Leu
 2435 2440 2445
 Thr Ala Ala Gly Thr Thr Ser Ala Thr Pro Asp Gly Ala Pro Glu Leu
 2450 2455 2460
 10 Ala Arg Arg Leu Ser Met Leu Asn Glu Thr Glu Arg Leu Arg Lys Leu
 2465 2470 2475 2480
 Val Glu Leu Val Arg Thr Glu Ala Ala Phe Val Leu Arg His Pro Asn
 2485 2490 2495
 15 Thr Asp Ala Ile Gly Ala Glu Arg Pro Phe Lys Ser Ala Gly Phe Asp
 2500 2505 2510
 Ser Leu Thr Ser Leu Glu Leu Arg Asn Arg Leu Asn Ala Gly Thr Gly
 2515 2520 2525
 20 Leu Lys Leu Pro Ala Thr Val Ile Phe Asp His Pro Ser Pro Thr Ala
 2530 2535 2540
 Leu Ala Arg Leu Leu Leu Asp Arg Leu Thr Gly Ala Gly Ala Pro Ala
 2545 2550 2555 2560
 25 Pro Ala Ala Asp Glu Pro Pro Leu Pro Val Ala Val Ala Asp Asp Asp
 2565 2570 2575
 Pro Val Val Ile Val Gly Met Ala Cys Arg Phe Pro Gly Gly Ala Gly
 30 2580 2585 2590
 Thr Pro Glu Ala Leu Trp Lys Leu Val Thr Glu Glu Arg Asp Val Ile
 2595 2600 2605
 Gly Ala Ala Pro Thr Asp Arg Gly Trp Asp Leu Asp Ser Val Tyr Asp
 35 2610 2615 2620
 Pro Glu Pro Gly Val Ala Gly Lys Thr Tyr Val Arg Glu Gly Gly Phe
 2625 2630 2635 2640
 40 Leu His Asp Ala Ala Glu Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro
 2645 2650 2655
 Arg Glu Ala Val Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr
 2660 2665 2670
 45 Ser Trp Glu Ala Ile Glu Arg Ala Gly Ile Asp Pro His Ser Leu His
 2675 2680 2685
 Gly Ser Arg Thr Gly Val Tyr Val Gly Leu Thr His Gln Glu Tyr Ala
 50 2690 2695 2700
 Ser Arg Leu His Glu Ala Pro Glu Glu Tyr Glu Gly Tyr Leu Leu Thr
 2705 2710 2715 2720
 Gly Lys Ser Ala Ser Val Val Ser Gly Arg Ile Ser Tyr Thr Leu Gly
 55 2725 2730 2735

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Leu Glu Gly Pro Ser Leu Ser Ile Asp Thr Ala Cys Ser Ser Ser Leu
 2740 2745 2750

5 Val Ala Leu His Asn Ala Ala Gln Ala Leu Arg Gly Gly Glu Cys Asp
 2755 2760 2765

Met Ala Leu Ala Gly Gly Val Thr Val Met Ala Ala Pro Gly Leu Phe
 2770 2775 2780

10 Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Ala Asp Gly Arg Cys Lys
 2785 2790 2795 2800

Ala Phe Ala Asp Gly Ala Asp Gly Thr Ala Trp Ala Glu Gly Ala Gly
 2805 2810 2815

15 Val Val Leu Val Glu Arg Leu Ser Asp Ala Arg Arg Leu Gly His Pro
 2820 2825 2830

Val Leu Ala Val Val Cys Gly Ser Ala Val Asn Gln Asp Gly Ala Ser
 2835 2840 2845

20 Asn Gly Leu Thr Ala Pro Ser Gly Pro Ser Gln Glu Arg Val Ile Arg
 2850 2855 2860

Gln Ala Leu Ala Asn Ala Arg Leu Thr Val Ala Asp Val Asp Val Val
 2865 2870 2875 2880

25 Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln
 2885 2890 2895

Ala Leu Leu Gly Thr Tyr Gly Arg Asp Arg Asp Ala Glu Cys Pro Val
 2900 2905 2910

30 Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln Ala Ala Ala
 2915 2920 2925

Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Met Arg Tyr Gly Trp
 35 2930 2935 2940

Leu Pro Arg Thr Leu His Val Asp Glu Pro Ser Arg His Val Asp Trp
 2945 2950 2955 2960

40 Ser Ala Gly Gly Val Arg Leu Leu Thr Glu Ala Arg Glu Trp Pro Gly
 2965 2970 2975

Val Asp Arg Pro Arg Arg Ala Ala Val Ser Ala Phe Gly Val Ser Gly
 2980 2985 2990

45 Thr Asn Ala His Leu Ile Leu Glu Ala Pro Glu Ala Leu Glu Ala Leu
 2995 3000 3005

Glu Ala Thr Asp Ala Pro Glu Ala Pro Glu Ala Pro Glu Ala Pro Asp
 50 3010 3015 3020

Val Thr Asp Val Thr Glu Ala Leu Glu Ala Pro Asp Ala Thr Glu Ala
 3025 3030 3035 3040

Glu Gly Ala Lys Ala Pro Gly Ser Pro Glu Glu Ala Gln Pro Ala Val
 55 3045 3050 3055

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Gly Val Val Pro Val Val Ser Gly Arg Ser Arg Val Val Val Arg
 3060 3065 3070

5 Glu Ala Ala Gly Arg Leu Ala Glu Val Val Glu Ala Gly Gly Val Gly
 3075 3080 3085

Leu Ala Asp Val Ala Val Thr Met Ala Gly Arg Ser Arg Phe Gly Tyr
 3090 3095 3100

10 Arg Ala Val Val Leu Ala Arg Gly Glu Ala Glu Leu Ala Gly Arg Leu
 3105 3110 3115 3120

Arg Ala Leu Ala Gly Gly Asp Pro Asp Ala Gly Val Val Thr Gly Ala
 3125 3130 3135

15 Val Val Asp Pro Glu Thr Gly Ser Gly Gly Val Val Leu Val
 3140 3145 3150

Phe Pro Gly Gln Gly Thr Gln Trp Val Gly Met Gly Ala Gly Leu Leu
 3155 3160 3165

20 Gly Ser Ser Glu Val Phe Ala Ala Ser Met Arg Glu Cys Ala Arg Ala
 3170 3175 3180

Leu Ser Val His Val Glu Trp Asp Leu Leu Glu Val Val Ser Gly Gly
 3185 3190 3195 3200

25 Ala Gly Leu Glu Arg Val Asp Val Val Gln Pro Val Thr Trp Ala Val
 3205 3210 3215

Met Val Ser Leu Ala Arg Tyr Trp Gln Ala Met Gly Val Asp Val Ala
 3220 3225 3230

30 Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala Thr Val Ala
 3235 3240 3245

Gly Ala Leu Ser Leu Glu Asp Ala Ala Ala Val Val Ala Leu Arg Ala
 3250 3255 3260

35 Gly Leu Ile Gly Arg Tyr Leu Ala Gly Arg Gly Ala Met Ala Ala Val
 3265 3270 3275 3280

40 Pro Leu Pro Ala Gly Glu Val Glu Ala Gly Leu Ala Lys Trp Pro Gly
 3285 3290 3295

Val Gln Val Ala Ala Val Asn Gly Pro Ala Ser Thr Val Val Ser Gly
 3300 3305 3310

45 Asp Arg Arg Ala Val Ala Gly Tyr Val Ala Val Cys Gln Ala Glu Gly
 3315 3320 3325

Val Gln Ala Arg Leu Ile Pro Val Asp Tyr Ala Ser His Ser Arg His
 3330 3335 3340

50 Val Glu Asp Leu Lys Gly Glu Leu Glu Arg Val Leu Ser Gly Ile Arg
 3345 3350 3355 3360

Pro Arg Ser Pro Arg Val Pro Val Cys Ser Thr Val Ala Gly Glu Gln
 55 3365 3370 3375

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Pro Gly Glu Pro Val Phe Asp Ala Gly Tyr Trp Phe Arg Asn Leu Arg
 3380 3385 3390
 Asn Arg Val Glu Phe Ser Ala Val Val Gly Gly Leu Leu Glu Gln Gly
 5 3395 3400 3405
 His Arg Arg Phe Ile Glu Val Ser Ala His Pro Val Leu Val His Ala
 3410 3415 3420
 Ile Glu Gln Thr Ala Glu Ala Ala Asp Arg Ser Val His Ala Thr Gly
 10 3425 3430 3435 3440
 Thr Leu Arg Arg Gln Asp Asp Ser Pro His Arg Leu Leu Thr Ser Thr
 3445 3450 3455
 Ala Glu Ala Trp Ala His Gly Ala Thr Leu Thr Trp Asp Pro Ala Leu
 15 3460 3465 3470
 Pro Pro Gly His Leu Thr Thr Leu Pro Thr Tyr Pro Phe Asn His His
 3475 3480 3485
 His Tyr Trp Ala Val Thr Ser Pro Ala Gly Val Gly Asp Ala Ala Ala
 20 3490 3495 3500
 Gly Arg Phe Gly Met Thr Trp Glu Asp His Pro Phe Leu Arg Gly Gly
 25 3505 3510 3515 3520
 Leu Pro Leu Ala Asp Ser Gly Glu Arg Val Phe Ala Gly Arg Leu Ala
 3525 3530 3535
 Gly Ser Glu His Asp Trp Leu Thr Asp His Ala Val Ser Gly Val Thr
 30 3540 3545 3550
 Leu Leu Pro Gly Thr Ala Phe Val Glu Phe Ala Leu His Ala Gly Ala
 3555 3560 3565
 Ala Thr Gly Cys Gly Arg Leu Glu Glu Leu Ser Val Glu Ala Pro Leu
 35 3570 3575 3580
 Val Leu Pro Ala Ala Gly Gly Val Arg Val Gln Met Arg Val Ser Ala
 3585 3590 3595 3600
 Ala Asp Glu Ser Gly Arg Arg Arg Val Ala Ile His Ser Ala Pro Glu
 40 3605 3610 3615
 Ala Ala Val His Ser Ala Ala Glu Gly Gly Asp Ser Ala Gly Val Trp
 3620 3625 3630
 Thr Arg His Gly Glu Gly Thr Leu Val Pro Asp Pro Glu Pro Thr Pro
 45 3635 3640 3645
 Pro Asp Ala Asp Trp Ala Arg Ala Trp Pro Pro Ala Gly Glu Arg Val
 3650 3655 3660
 50 Glu Pro Ala Glu Leu Tyr Glu Arg Phe Gly Ala Leu Gly Tyr Glu Tyr
 3665 3670 3675 3680
 Gly Glu Ala Phe Ala Gly Val Arg Ala Val Trp Arg Gln Pro Asp Ala
 55 3685 3690 3695

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Leu Leu Ala Glu Val Leu Leu Pro Asp Arg Ala Ser Thr Gly Ala Gly
 3700 3705 3710
 Arg Phe Gly Val His Pro Ala Leu Leu Asp Ala Ala Leu Gln Pro Trp
 5 3715 3720 3725
 Ile Ala Gly Gly Leu Leu Glu Val Pro Glu Asp Ala Val Leu Leu Pro
 3730 3735 3740
 Phe Ala Trp Gln Gly Val Ser Leu Tyr Ala Thr Gly Ala Gly Ala Leu
 10 3745 3750 3755 3760
 Arg Val Arg Leu Thr Lys Ala Gly Asp Gly Ala Val Ser Leu Gln Ala
 3765 3770 3775
 Ala Asp Thr Ser Gly Ala Ala Val Leu Ser Leu Gly Ala Leu Val Met
 15 3780 3785 3790
 Arg Pro Leu Ala Arg Arg Lys Leu Asp Val Leu Leu Gly Thr Asp Ala
 3795 3800 3805
 20 Gly Glu Arg Ser Leu Tyr Arg Val Glu Trp Gln Pro Arg Leu Leu Pro
 3810 3815 3820
 Ala Gly Pro Pro Arg Ser Trp Ala Val Leu Gly Pro Asp Ala Asp Arg
 25 3825 3830 3835 3840
 Leu Ala Gly Thr Pro Gly Leu Gly Asp Gln Pro Asp Gly Gly Pro Thr
 3845 3850 3855
 Ala Leu Tyr Pro Glu Val Arg Ala Leu Arg Lys Ala Leu Ala Ala Gly
 30 3860 3865 3870
 Ala Pro Arg Pro Glu Ala Val Val Leu Pro Val Leu Ser Gly Ala Gly
 3875 3880 3885
 Ala Thr Pro Glu Ser Val Arg Gln Thr Thr Glu Arg Cys Leu Thr Ala
 35 3890 3895 3900
 Leu Gln Asp Trp Leu Asp Ala Glu Glu Leu Val Asp Thr Pro Leu Ile
 40 3905 3910 3915 3920
 Val Leu Thr Arg Gly Ala Val Ala Ala Val Pro Gly Glu Glu Ile Gly
 3925 3930 3935
 Asp Leu Ala Cys Ala Gly Val Trp Gly Leu Val Arg Ser Ala Arg Ser
 45 3940 3945 3950
 Glu His Pro Gly Arg Phe Ala Leu Val Asp Thr Asp Gly His Pro Asp
 3955 3960 3965
 Asp Arg Thr Ala Leu Pro Leu Ala Leu Arg Ala Val Leu Asp Gly Ala
 50 3970 3975 3980
 Gly Gln Leu Ser Leu Arg Ala Gly Thr Ala Arg Thr Pro Val Leu Leu
 3985 3990 3995 4000
 Arg Ala Gly Thr Pro Glu Glu Gln Arg Gly Pro Ala Phe Asp Pro Ala
 55 4005 4010 4015

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Gly Thr Val Leu Val Thr Gly Ala Thr Gly Thr Leu Gly Arg Leu Leu
 4020 4025 4030

5 Ala Arg His Leu Ala Ala Glu His Gly Val Arg His Leu Leu Leu Leu
 4035 4040 4045

Ser Arg Gly Gly Arg Ala Ala Glu Gly Ala Asp Glu Leu Ala Ala Glu
 4050 4055 4060

10 Leu Ala Gly Leu Glu Ala Glu Pro Cys Phe Ala Ala Cys Asp Ala Ala
 4065 4070 4075 4080

Asp Arg Glu Ala Leu Ala Arg Val Leu Ala Glu Val Pro Ala Asp Arg
 4085 4090 4095

15 Pro Leu Thr Gly Val Ile His Ala Ala Gly Val Leu Asp Asp Gly Thr
 4100 4105 4110

Leu Asp Ala Leu Thr Pro Glu Arg Ile Gly Thr Val Met Arg Pro Lys
 4115 4120 4125

20 Ala Asp Ala Ala Leu Asn Leu His Glu Leu Thr Arg Thr Ser Pro Leu
 4130 4135 4140

Ser Val Phe Ala Val Phe Ser Gly Ala Ala Gly Ile Leu Gly Arg Pro
 4145 4150 4155 4160

25 Gly Gln Ala Asn Tyr Ala Ala Ala Asn Thr Phe Leu Asp Ala Leu Ala
 4165 4170 4175

Gln His Arg Arg Ala His Gly Leu Pro Ala Val Ser Leu Ala Trp Gly
 30 4180 4185 4190

Leu Trp Gly Gly Ala Thr Gly Met Thr Gly His Leu Ser Gly Thr Asp
 4195 4200 4205

Leu Arg Arg Met Arg Arg Ser Gly Ile Ala Pro Met Thr His Asp Gln
 35 4210 4215 4220

Gly Leu Ala Leu Phe Asp Arg Ala Leu Ala Ala Ser Ala Glu Asp Pro
 4225 4230 4235 4240

40 Leu Leu Val Pro Met Arg Leu Asp Leu Ala Ala Leu Val Arg Glu Arg
 4245 4250 4255

Ala Glu His Gly Pro Asp Ala Val Pro Gly Pro Leu Leu Gly Leu Leu
 4260 4265 4270

45 Pro Ala Arg Ala Ala Val Arg Gln Ala Ala Ala Pro Val Arg Gly Gly
 4275 4280 4285

Ala Pro Ala Pro Ala Gly Gly Glu Gly Thr Ala Glu Arg Leu Ala Gly
 50 4290 4295 4300

Leu Gly Glu Glu Ala Arg Leu Arg Glu Leu Val Arg Leu Val Arg Ala
 4305 4310 4315 4320

Glu Val Ser Gly Val Leu Gly Tyr Ser Gly Pro Asp Ala Val Glu Pro
 55 4325 4330 4335

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Gly Arg Pro Phe Lys Asp Leu Gly Phe Asp Ser Leu Thr Ala Val Glu
4340 4345 4350

5 Leu Arg Asn Arg Leu Gly Ala Ala Thr Gly Leu Arg Leu Pro Thr Ala
4355 4360 4365

Leu Val Phe Asp Arg Pro Thr Ser Gln Ala Val Ala Glu Tyr Leu Ala
4370 4375 4380

10 Ala Glu Leu Ala Gly Pro Arg Asp Gly Gly Asp Thr Ala Ala Ala Ala
4385 4390 4395 4400

Phe Glu Gly Leu Glu Ala Leu Ala Ala Val Gly Ala Leu Ala Glu
4405 4410 4415

15 Asp Asp Leu Arg Arg Asp Val Leu Arg Arg Leu Thr Glu Leu Ala
4420 4425 4430

Ala Ala Leu Thr Pro Gln Gly Arg Asn Pro Ser Ala Pro Ala Pro Ala
4435 4440 4445

20 Pro Ser Asp Leu Asp Glu Arg Leu Asp Ser Ala Asn Asp Asp Asp Leu
4450 4455 4460

25 Phe Ala Phe Ile Glu Glu Gln Leu *
4465 4470

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1865 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Ala Glu Leu Val Ala Thr Arg Lys Arg Leu Gly Ala Leu Glu
1 5 10 15

40 Glu Arg Ala Arg Glu Pro Ile Ala Val Val Ala Met Ser Cys Arg Tyr
20 25 30

Pro Gly Gly Val Thr Thr Pro Glu Asp Leu Trp Arg Leu Leu Ala Asp
35 40 45

45 Glu Arg Asp Ala Val Ser Gly Leu Pro Arg Asp Arg Gly Trp Asp Leu
50 55 60

50 Asp Ala Leu Tyr Asp Pro Asp Gly Gly Pro Gly Thr Ser Tyr Ala Arg
65 70 75 80

Glu Gly Gly Phe Leu Ser His Cys Ala Gly Phe Asp Ala Glu Phe Phe
85 90 95

55 Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu
100 105 110

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Leu Leu Glu Thr Ser Trp Glu Ala Leu Glu Arg Ala Gly Val Thr Ala
 115 120 125
 Asp Arg Ala Arg Gly Ser Arg Thr Gly Val Tyr Ala Gly Val Met Tyr
 5 130 135 140
 Asp Asp Tyr Gly Ala Arg Val Leu Tyr Gly Ala Gly Ala Gly Pro Pro
 145 150 155 160
 Glu Asp Leu Glu Gly Tyr Leu Val Asn Gly Ser Ala Gly Ser Ile Ala
 10 165 170 175
 Ser Gly Arg Val Ser Tyr Thr Phe Gly Leu Arg Gly Pro Ala Val Thr
 180 185 190
 Val Asn Thr Ala Cys Ser Ser Ser Leu Val Ser Leu His Leu Ala Val
 195 200 205
 Arg Ala Leu Arg Asn Gly Glu Cys Asp Met Ala Leu Ala Gly Gly Ala
 210 215 220
 20 Thr Val Leu Ser Thr Pro Thr Val Leu Val Asp Phe Ser Arg Gln Arg
 225 230 235 240
 Gly Leu Ala Pro Asp Gly Arg Cys Lys Ala Phe Ala Asp Ser Ala Asp
 25 245 250 255
 Gly Thr Ser Trp Ala Glu Gly Ala Gly Met Leu Leu Leu Gln Arg Leu
 260 265 270
 Ser Asp Ala Arg Arg Glu Gly Arg Pro Val Leu Ala Val Ile Arg Gly
 30 275 280 285
 Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn
 290 295 300
 Gly Arg Ala Gln Arg Gln Val Ile Glu Asp Ala Leu Arg Asp Ala Gly
 35 305 310 315 320
 Val Gly Pro Asp Gin Val Asp Ala Val Glu Ala His Gly Thr Gly Thr
 325 330 335
 Glu Leu Gly Asp Pro Ile Glu Ala Gly Ala Leu Leu Ala Thr Tyr Gly
 40 340 345 350
 Thr Ala Arg Thr Ala Glu Arg Pro Leu Trp Leu Gly Ser Leu Lys Ser
 355 360 365
 45 Asn Ile Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys
 370 375 380
 Met Val Leu Ala Met Arg His Gly Arg Leu Pro Arg Thr Leu His Val
 385 390 395 400
 50 Asp Arg Pro Thr Thr Arg Val Asp Trp Glu Lys Gly Gly Val Arg Leu
 405 410 415
 Leu Thr Glu Pro Val Pro Trp Pro Gly Glu Ala Gly Glu Pro Arg Arg
 55 420 425 430

EP 0791 655 A2

Ala Gly Val Ser Ser Phe Gly Ala Ser Gly Thr Asn Ala His Val Val
 435 440 445
 Leu Glu Ser Val Pro Ala Gly Glu Pro Pro Ala Ala Gly Arg Pro Glu
 5 450 455 460
 Asp Thr Gly Gly Ala Trp Thr Val Ser Gly Arg Gly Pro Ala Ala Leu
 465 470 475 480
 Arg Ala Gln Ala Ala Arg Leu Tyr Asp Ala Leu Thr Gly Thr Gly Thr
 10 485 490 495
 Gly Thr Gly Gln Gly Ala Gly Gln Gly Ala Gly Pro Gly Thr Ala Glu
 500 505 510
 Val Ala Gly Ala Leu Ala His Ala Arg Thr Ala Phe Arg His Arg Ala
 15 515 520 525
 Val Val Leu Gly Gly Asn Arg Ala Glu Leu Leu Ala Gly Leu Arg Glu
 530 535 540
 20 Leu Ala Glu Glu Glu His Pro Gly Pro Arg Val Val Thr Gly Thr Ala
 545 550 555 560
 Pro Ala Thr Glu Arg Arg Thr Ala Phe Leu Phe Ser Gly Gln Gly Ser
 565 570 575
 25 Gln Arg Ala Gly Ser Gly Arg Gly Leu Tyr Arg Arg His Pro Val Phe
 580 585 590
 Ala Arg Ala Leu Asp Glu Val Cys Ala Ala Leu Glu Pro His Leu His
 30 595 600 605
 Arg Pro Leu Arg Asp Leu Met Phe Ala Glu Pro Gly Ser Pro Glu Ala
 610 615 620
 35 Glu Pro Leu Asp Arg Thr Glu Phe Thr Gln Pro Ala Leu Phe Ala Leu
 625 630 635 640
 Gln Thr Ala Leu Phe Arg Leu Ala Glu His His Gly Leu Arg Ala Glu
 40 645 650 655
 Ala Leu Cys Gly His Ser Val Gly Glu Ile Ala Ala Ala His Ala Ala
 660 665 670
 Gly Val Leu Thr Leu Pro Asp Ala Ala Arg Leu Val Ala Ala Arg Gly
 45 675 680 685
 Arg Leu Met Gln Ala Leu Pro Ala Gly Gly Ala Met Ala Ala Leu Arg
 690 695 700
 Ala Thr Ala Glu Glu Ile Ala Pro Leu Leu Glu Arg Arg Ala Gly Glu
 50 705 710 715 720
 Leu Ala Leu Ala Ala Val Asn Gly Pro Ser Ser Val Val Val Ser Gly
 725 730 735
 Asp Glu Ala Ala Val Leu Glu Leu Leu Glu Gln Trp Arg Ala Glu Gly
 55 740 745 750

EP 0 791 655 A2

Arg Glu Ala Arg Arg Leu Ala Val Ser His Ala Phe His Ser Pro Arg
 755 760 765
 Met Asp Gly Met Leu Thr Gln Phe Asp Arg Val Ala Arg Thr Leu Thr
 5 770 775 780
 Phe Ala Pro Pro Thr Ile Pro Leu Val Ser Thr Leu Thr Gly Thr Pro
 785 790 795 800
 Val Thr Glu Glu Thr Leu Cys Thr Ala Asp His Trp Val Arg Gln Ala
 10 805 810 815
 Arg Glu Pro Val Arg Phe Leu Asp Ala Met Arg Thr Leu Arg Ala Asp
 820 825 830
 Gly Ile Asp Thr Phe Val Glu Leu Gly Pro Asp Gly Val Leu Ser Ala
 15 835 840 845
 Met Ala Arg Asp Cys Ala Asp Asp Arg Pro Asp Gly Asp Thr Thr Gly
 850 855 860
 Ala Gly Asp Gly Glu Thr Pro Asp Pro Leu Leu Thr Leu Pro Leu Leu
 20 865 870 875 880
 Arg Arg Ser Val Pro Glu Thr Gly Asp Ala Glu His Pro Gly Gly Phe
 885 890 895
 25 Glu Arg Ala Leu Ala Thr Ala Tyr Ala His Gly Val Pro Leu Arg Leu
 900 905 910
 Ala Pro Ala Pro Asp Ala Ala Ser Leu Ala Val Ala Ala Glu Leu Pro
 915 920 925
 Thr Tyr Ala Phe Gln Arg Thr His Tyr Trp Leu Asp Ala Pro Ala Ala
 30 930 935 940
 Pro Ala Ala Leu Pro Ala Gly Leu Asp Asp Ala Gly His Pro Leu Leu
 35 945 950 955 960
 Ser Ala Ala Leu Asp Leu Pro Gly Gly Arg Gly Thr Val Trp Thr Gly
 965 970 975
 Ala Leu Ser Ala Ala Thr Leu Pro Trp Ala Ala Asp His Ser Val His
 40 980 985 990
 Gly Arg Thr Val Leu Pro Gly Thr Ala Leu Leu Asp Leu Ala Leu His
 995 1000 1005
 Ala Ala Pro Arg Val Gly Glu Leu Thr Phe Glu Ala Pro Leu Val Leu
 45 1010 1015 1020
 Pro Glu Asp Gly Glu Val Arg Leu Arg Val Val Leu Ala Glu Pro Asp
 1025 1030 1035 1040
 50 Ala Ser Gly Val Arg Glu Leu Ser Val His Ser Ala Gly Glu Asp Gly
 1045 1050 1055
 Gly Trp Thr Arg His Ala Thr Ala Val Leu Asp Thr Gly Thr Thr Thr
 55 1060 1065 1070

EP 0 791 655 A2

Ala Gly Glu Pro Ala Gly Ala Pro Pro Ala Ala Trp Pro Pro Gly Asp
 1075 1080 1085
 5 Ala Glu Pro Leu Asp Leu Ala Ala Glu Tyr Glu Arg Phe Ala Asp Ala
 1090 1095 1100
 Gly Ile Gly Tyr Gly Pro Ala Phe Arg Gly Leu Arg Ser Ala Trp Arg
 1105 1110 1115 1120
 10 Asp Gly Asp Ala Ile Leu Ala Asp Val Arg Leu Pro Gly Glu Leu Ala
 1125 1130 1135
 Gly Glu Ala Asp Arg Tyr Gly Ile His Pro Ala Leu Leu Asp Ala Ala
 1140 1145 1150
 15 Leu His Thr Ala Ala Ala Leu Gly Gly Ala His Gly Met Leu Pro
 1155 1160 1165
 Phe Thr Trp Asn Gly Val Thr Leu His Ala Arg Gly Ala His Ala Ile
 1170 1175 1180
 20 Arg Val Arg Leu Thr Pro Ala Gly Pro Asp Ala Val Ala Val Thr Ala
 1185 1190 1195 1200
 Val Asp Pro Ala Gly Arg Pro Val Phe Thr Ala Ala Ser Leu Thr Leu
 1205 1210 1215
 25 Arg Pro Val Thr Thr Gly Gln Leu Thr Ala Ala Glu Ala Ala Arg Ala
 1220 1225 1230
 Pro Leu Tyr Arg Val Arg Trp Thr Gly Leu Pro Asp Thr Gly Thr Ala
 1235 1240 1245
 30 Arg Asp His Thr Trp Ala Val Ala Gly Gly Pro Gly Asp Leu Leu Pro
 1250 1255 1260
 Gly Glu Thr Pro His His Pro Asp Leu Ala Ser Ala Leu Ala Asp Thr
 1265 1270 1275 1280
 35 Gly Thr Ala Pro Phe Arg Val Leu Ala Asp Leu Arg Gly Tyr Gly Thr
 1285 1290 1295
 Ala Thr Pro Arg Glu Leu Ala Ser Gln Ala Leu Ala Leu Val Gln Gln
 40 1300 1305 1310
 Trp Ala Asp Ala Ala Glu Ala Ala Glu Gly Arg Leu Val Leu Val Thr
 1315 1320 1325
 45 Arg Arg Ala Val Asp Ile Gly Asp Gly Val Thr Asp Pro Ala Ala Ala
 1330 1335 1340
 Thr Val Trp Gly Leu Val Arg Ala Ala Gln Ser Glu His Pro Gly Cys
 1345 1350 1355 1360
 50 Phe Ala Leu Leu Asp Thr Asp Asp Ser Pro Arg Ser Arg Gln Leu Leu
 1365 1370 1375
 Pro Arg Val Ala Gly Thr Ala Glu Gln Leu Ala Leu Arg Asp Gly Thr
 55 1380 1385 1390

EP 0791 655 A2

Leu Leu Ala Pro Ser Leu Thr Arg Ala Thr Leu Pro Ala Gly Ala Arg
 1395 1400 1405
 5 Leu Pro Ala Leu Asp Gly Thr Val Leu Ile Thr Gly Gly Thr Gly Ser
 1410 1415 1420
 Leu Gly Ala Glu Ala Ala Arg His Leu Val Thr Arg His Gly Ala Arg
 1425 1430 1435 1440
 10 Arg Leu Leu Leu Thr Ser Arg Ser Gly Pro Gln Ala Pro Gly Ala Ala
 1445 1450 1455
 Glu Leu Val Ala Glu Leu Ala Ala Leu Gly Ala His Ala Asp Val Ala
 1460 1465 1470
 15 Ala Cys Asp Val Ala Asp Arg Ala Ala Leu Arg Ala Leu Leu Asp Arg
 1475 1480 1485
 Val Pro Ala Gly His Pro Leu Thr Ala Val Leu His Thr Ala Gly Val
 1490 1495 1500
 20 Leu Asp Asp Gly Val Leu Thr Ala Gln Thr Pro Gln Arg Leu Ala Ala
 1505 1510 1515 1520
 Val Leu Arg Pro Lys Ala Asp Ala Val Arg Asn Leu His Glu Leu Thr
 1525 1530 1535
 25 Gln Gly His Ala Leu Ser Ala Phe Ile Leu Tyr Ser Ser Ala Ala Gly
 1540 1545 1550
 Val Leu Gly Ser Ala Gly Gln Ser Gly Tyr Ala Ala Ala Asn Ala Tyr
 1555 1560 1565
 30 Leu Asp Ser Phe Ala Val Trp Arg Arg Ser Arg Gly Leu Pro Ala Val
 1570 1575 1580
 Ser Leu Gly Trp Gly Pro Trp Asp Gly Gly Met Ala Ser Gly Leu
 35 1585 1590 1595 1600
 Gly Gly Thr Asp Thr Ala Arg Leu Arg Arg Ser Gly Ile Ala Pro Leu
 1605 1610 1615
 40 Ser Arg Ala Glu Gly Leu Ala Ala Leu Asp Ala Ala Leu Ala Ala Gly
 1620 1625 1630
 Gly Asp Asp Thr Ala Pro Ala His Leu Leu Pro Ile Arg Val Asp Ala
 1635 1640 1645
 45 Val Thr Leu Arg Gly Ala Asp Thr Val Pro Ala Val Leu Arg Asp Leu
 1650 1655 1660
 Ala Gly Thr Ala Pro Ser Ala Ala Glu Arg Pro Pro Gly Thr Pro Glu
 1665 1670 1675 1680
 50 Asp Thr Asn Ala Pro Leu Ala Asp Val Thr Gln Leu His Gly Arg Glu
 1685 1690 1695
 Arg Lys Glu Ala Leu Thr Gly Phe Val Arg Ala Gln Val Ala Ala Val
 55 1700 1705 1710

Leu Gly His Pro Thr Ser Asp Thr Ile Asp Val Arg Arg Ser Phe Lys
 1715 1720 1725
 Glu Ala Gly Phe Asp Ser Leu Thr Ala Val Glu Leu Arg Asn Arg Leu
 5 1730 1735 1740
 Arg Ala Ala Thr Gly Leu Lys Leu Pro Ala Thr Leu Val Phe Asp His
 1745 1750 1755 1760
 Pro Thr Pro Leu Ala Leu Ala Gly Phe Leu His Arg Glu Leu Pro Gly
 10 1765 1770 1775
 Ala Glu Ala Ser Leu Met Ser Ala Ile Asp Thr Leu Arg His Arg Leu
 1780 1785 1790
 Arg Asp Ala Leu Ala Asp Asp Ala Ala Asp Asp Ala Leu Arg Asp Gln
 15 1795 1800 1805
 Ile Thr Arg Arg Leu Glu Thr Leu Leu Ala Gly Ile Ala Arg Thr Glu
 1810 1815 1820
 Glu Pro Ala Pro Ala Thr Ala Ala Asp Asp Gly Ser Gly Ala Gly
 20 1825 1830 1835 1840
 Asp Val Ala Glu Arg Leu Ser Thr Ala Ser Asp Asp Glu Leu Phe Glu
 25 1845 1850 1855
 Leu Leu Asp Ser Gly Phe Thr Pro *
 1860 1865

30 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3730 amino acids
 (B) TYPE: amino acid
 35 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
 40 Met Ser Thr Glu Asn Ser Thr Asn Val Pro Ala Ser Glu Asp Lys Leu
 1 5 10 15
 Arg Ala Tyr Leu Arg Arg Ala Met Ala Asp Leu His Glu Ser Arg Glu
 45 20 25 30
 Arg Leu Arg Ala Thr Glu Ala Arg Ala Gln Glu Pro Ile Ala Val Val
 35 40 45
 Gly Met Gly Cys Arg Phe Pro Gly Gly Val Gly Ser Pro Glu Ala Leu
 50 55 60
 Trp Arg Leu Val Val Glu Gly Val Asp Ala Val Ser Pro Phe Pro Gly
 65 70 75 80
 Asp Arg Gly Trp Asp Val Glu Gly Leu Tyr Asp Pro Glu Pro Gly Val
 55 85 90 95

Ala Gly Lys Ser Tyr Val Arg Glu Gly Gly Phe Leu His Asp Ala Ala
 100 105 110
 5 Glu Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg Glu Ala Val Ala
 115 120 125
 Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr Ser Trp Glu Ala Ile
 130 135 140
 10 Glu Arg Ala Gly Ile Asp Pro His Ser Leu His Gly Ser Arg Thr Gly
 145 150 155 160
 Val Tyr Ala Gly Val Met Tyr His Asp Tyr Gly Thr Gly Gln Thr Ser
 165 170 175
 15 Ala Thr Asp Thr Ser Gly Tyr Ser Gly Thr Gly Thr Ser Gly Ser Val
 180 185 190
 Val Ser Gly Arg Val Ala Tyr Thr Leu Gly Leu Glu Gly Pro Ala Val
 20 195 200 205
 Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala
 210 215 220
 25 Val Gln Ala Leu Arg Gly Gly Glu Cys Asp Met Ala Leu Ala Gly Gly
 225 230 235 240
 Val Thr Val Met Ala Gly Pro Gly Met Phe Val Glu Phe Ser Arg Gln
 245 250 255
 30 Arg Gly Leu Ala Ala Asp Gly Arg Cys Lys Ala Phe Ala Asp Gly Ala
 260 265 270
 Asp Gly Thr Ala Trp Ala Glu Gly Ala Gly Val Val Leu Val Glu Arg
 275 280 285
 35 Leu Ser Asp Ala Arg Arg Leu Gly His Pro Val Leu Ala Val Val Cys
 290 295 300
 Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro
 305 310 315 320
 40 Ser Gly Pro Ser Gln Glu Arg Val Ile Arg Gln Ala Leu Ala Asn Ala
 325 330 335
 Arg Leu Thr Val Ala Asp Val Asp Val Val Glu Ala His Gly Thr Gly
 45 340 345 350
 Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Leu Gly Thr Tyr
 355 360 365
 50 Gly Arg Asp Arg Asp Gly Gly Arg Pro Val Trp Leu Gly Ser Leu Lys
 370 375 380
 Ser Asn Ile Gly His Ala Gln Ala Ala Gly Val Ala Gly Val Ile
 385 390 395 400
 Lys Met Val Leu Ala Met Arg Tyr Gly Trp Leu Pro Arg Thr Leu His
 55 405 410 415

Val Asp Glu Pro Ser Arg His Val Asp Trp Ser Ala Gly Gly Val Trp
 420 425 430

5 Leu Leu Thr Glu Ala Arg Glu Trp Pro Gly Val Asp Arg Pro Arg Arg
 435 440 445

Ala Ala Val Ser Ala Phe Gly Val Ser Gly Thr Asn Ala His Leu Ile
 450 455 460

10 Leu Glu Ala Pro Asp Thr Ala Glu Ala Glu Ser Ala Thr Thr Pro Val
 465 470 475 480

Arg Ser Glu Val Ser Glu Ser Ala Ala Val Phe Asp Ala Arg Ser Gly
 485 490 495

15 Val Val Pro Val Val Ser Gly Arg Ser Arg Val Val Val Arg Glu
 500 505 510

Ala Ala Gly Arg Leu Ala Glu Val Val Glu Ala Gly Gly Val Gly Leu
 20 515 520 525

Ala Asp Val Ala Val Thr Met Ala Gly Arg Ser Arg Phe Gly Tyr Arg
 530 535 540

25 Ala Val Val Leu Ala Arg Gly Glu Ala Glu Leu Ala Gly Arg Leu Arg
 545 550 555 560

Ala Leu Ala Gly Gly Asp Pro Asp Ala Gly Val Val Thr Gly Ala Val
 565 570 575

30 Val Asp Pro Glu Thr Gly Ser Gly Gly Val Val Leu Val Phe
 580 585 590

Pro Gly Gln Gly Thr Gln Trp Val Gly Met Gly Ala Gly Leu Leu Gly
 595 600 605

35 Ser Ser Glu Val Phe Ala Ala Ser Met Arg Glu Cys Ala Arg Ala Leu
 610 615 620

Ser Val His Val Gly Trp Asp Leu Leu Glu Val Val Ser Gly Gly Ala
 625 630 635 640

40 Gly Leu Glu Arg Val Asp Val Val Gln Pro Val Thr Trp Ala Val Met
 645 650 655

Val Ser Leu Ala Arg Tyr Trp Gln Ala Met Gly Val Asp Val Ala Ala
 45 660 665 670

Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala Thr Val Ala Gly
 675 680 685

Ala Leu Ser Leu Glu Asp Ala Ala Ala Val Val Ala Leu Arg Ala Gly
 50 690 695 700

Leu Ile Gly Arg Tyr Leu Ala Gly Arg Gly Ala Met Ala Ala Val Pro
 705 710 715 720

55 Leu Pro Ala Gly Glu Val Glu Ala Gly Leu Ala Lys Trp Pro Gly Val
 725 730 735

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Glu Val Ala Ala Val Asn Gly Pro Ala Ser Thr Val Val Ser Gly Asp
 740 745 750
 5 Arg Arg Ala Val Ala Gly Tyr Val Ala Val Cys Gln Ala Glu Gly Val
 755 760 765
 Gln Ala Arg Leu Ile Pro Val Asp Tyr Ala Ser His Ser Arg His Val
 770 775 780
 10 Glu Asp Leu Lys Gly Glu Leu Glu Arg Val Leu Ser Gly Ile Arg Pro
 785 790 795 800
 Arg Ser Pro Arg Val Pro Val Cys Ser Thr Val Ala Gly Glu Gln Pro
 805 810 815
 15 Gly Glu Pro Val Phe Asp Ala Gly Tyr Trp Phe Arg Asn Leu Arg Asn
 820 825 830
 Arg Val Glu Phe Ser Ala Val Val Gly Gly Leu Leu Glu Glu Gly His
 20 835 840 845
 Arg Arg Phe Ile Glu Val Ser Ala His Pro Val Leu Val His Ala Ile
 850 855 860
 25 Glu Gln Thr Ala Glu Ala Ala Asp Arg Ser Val His Ala Thr Gly Thr
 865 870 875 880
 Leu Arg Arg Gln Asp Asp Ser Pro His Arg Leu Leu Thr Ser Thr Ala
 885 890 895
 30 Glu Ala Trp Ala His Gly Ala Thr Leu Thr Trp Asp Pro Ala Leu Pro
 900 905 910
 Pro Gly His Leu Thr Thr Leu Pro Thr Tyr Pro Phe Asn His His His
 915 920 925
 35 Tyr Trp Leu Asp Thr Thr Pro Thr Thr Pro Ala Thr Thr Thr Gln Ser
 930 935 940
 Pro Thr Asp Ala Gln Asn Pro Ala Asp Ala Leu Pro Tyr Lys Val Ser
 945 950 955 960
 40 Trp Lys Arg Leu Arg Asp Gln Asp Ser Leu Thr Ala Arg Leu Asp Gly
 965 970 975
 Arg Trp Leu Leu Val Val Pro Glu Ala Ser Ala Asp Pro Ser Val Ala
 45 980 985 990
 Glu Gly Val Ala Arg Glu Leu Thr Ala Arg Gly Ala Thr Val Glu Ser
 995 1000 1005
 50 Leu Thr Val Glu Pro Gly Ala Asp Arg Ser Arg Leu Arg Gly Leu Leu
 1010 1015 1020
 Val Asp Ala Thr Glu Arg Asp Glu Ala Gly Pro Leu Arg Gly Ile Val
 1025 1030 1035 1040
 55 Ser Leu Leu Ala Leu Ala Gly Asp His Ala Gly Ala Asp Gly Ala Arg
 1045 1050 1055

Pro Val Val Pro Ala Gly Leu Ala Ala Ser Leu Ala Leu Ile Gln Ala
 1060 1065 1070
 5 Ala Gly Asp Ala Gly Thr Glu Ala Gly Leu Trp Ala Val Thr Arg Gly
 1075 1080 1085
 Ala Val Ala Ala Val Pro Gly Asp Val Pro Ala Pro Ser Gln Ala Leu
 1090 1095 1100
 10 Leu Trp Gly Phe Gly Arg Val Ala Gly Ile Glu Leu Pro His Cys Trp
 1105 1110 1115 1120
 Gly Gly Leu Leu Asp Leu Pro Thr Gly Pro Gly Asp Ser Gly Phe Arg
 1125 1130 1135
 15 Gln Leu Ala Ala Thr Leu Ala Gly Arg Pro Ala Glu Asp Gln Val Ala
 1140 1145 1150
 Leu Arg Ala Ser Gly Ala Tyr Gly Arg Arg Leu Val Arg Ala Ser Ala
 20 1155 1160 1165
 Ala Gly Gly Ala Asp Gly Trp Arg Pro Arg Gly Thr Val Leu Val Val
 1170 1175 1180
 25 Gly Asp Thr Ala Glu Val Ala Gly Pro Leu Val Arg Trp Leu Leu Gly
 1185 1190 1195 1200
 Asn Gly Ala Arg Arg Val Thr Leu Ser Gly Leu Ser Gly Pro Leu Pro
 1205 1210 1215
 30 Glu Glu Leu Ala Asp Val Ala Ala Arg Val Thr Val Ala Pro Cys Asp
 1220 1225 1230
 Pro Ala Asp Arg Pro Ala Leu Arg Thr Leu Leu Ala Glu Gln Ala Pro
 1235 1240 1245
 35 Thr Ala Val Leu Val Ala Pro Pro Ala Val Pro Pro Thr Pro Leu Ala
 1250 1255 1260
 Glu Met Thr Ala Glu Ala Leu Ala Ile Ala Leu Ser Ala Lys Thr Gly
 40 1265 1270 1275 1280
 Leu Val Asp Arg Leu Asp Ser Leu Leu Asp Glu Pro Asp Pro Leu Leu
 1285 1290 1295
 Glu Asp Gly Glu Leu Asp Ala Phe Val Val Phe Ser Ser Val Ala Gly
 45 1300 1305 1310
 Val Trp Gly Gly Ala Gly Gln Gly Gly Tyr Ala Ala Gly Thr Ala Tyr
 1315 1320 1325
 Leu Asp Ala Leu Ala Glu Cys Arg Arg Ala Gly Gly Leu Pro Val Thr
 50 1330 1335 1340
 Ser Val Ala Trp Thr Pro Trp Leu Gly Thr Pro Ala Ala Asp Ser Leu
 1345 1350 1355 1360
 55 Gly Glu Gln Met Ser Arg Ala Gly Ile Thr Pro Leu Asp Pro Ala Ala
 1365 1370 1375

Ser Leu Asp Ala Leu Ala Arg Ala Val Gly Arg Arg Ala Gly Cys Val
 1380 1385 1390
 5 Thr Val Ala Asp Ile Asp Trp Glu Arg Phe Ala Ser Ala Tyr Thr Ala
 1395 1400 1405
 Thr Arg Pro Thr Pro Met Phe Asp Glu Val Pro Glu Val Arg Arg Ile
 1410 1415 1420
 10 Gln Ala Ala Trp Ala Glu Ala Glu Ala Asp Ala Ala Arg Ser Gly Ala
 1425 1430 1435 1440
 Gly Gly Asp Ser Gln Leu Leu Arg Ser Leu Arg Gly Arg Pro Glu Glu
 1445 1450 1455
 15 Ala Gln Leu Ala Glu Leu Leu Arg Leu Val Arg Thr His Ala Ala Ala
 1460 1465 1470
 Val Leu Gly Leu Gly Ser Pro Gly Ala Val Glu Ala Arg Arg Ser Phe
 20 1475 1480 1485
 Lys Asp Leu Gly Phe Asn Ser Val Thr Ala Val Glu Leu Arg Asn Arg
 1490 1495 1500
 25 Leu Lys Glu Ala Thr Gly Leu Arg Leu Glu Val Ser Leu Val Phe Asp
 1505 1510 1515 1520
 His Pro Asp Pro Ala Ser Leu Ala Arg His Leu Leu Asp Leu Ala Leu
 1525 1530 1535
 30 Gly Gln Glu Pro Glu Glu Thr Pro Arg Ala Phe Ala Leu Glu Pro Ala
 1540 1545 1550
 Pro Asn Gly Glu Pro Ile Ala Ile Val Ser Met Ala Cys Arg Met Pro
 1555 1560 1565
 35 Gly Gly Val Ser Thr Pro Glu Glu Leu Trp Arg Leu Leu Arg Asp Gly
 1570 1575 1580
 Lys Asp Ala Ile Gly Pro Phe Pro Ala Asn Arg Gly Trp Asp Leu Glu
 40 1585 1590 1595 1600
 Asn Leu Tyr Asp Pro Asp Pro Asp Ala Asp Gly Arg Thr Tyr Val Arg
 1605 1610 1615
 45 Glu Gly Gly Phe Leu His Glu Ala Pro Asp Phe Asp Pro Ser Phe Phe
 1620 1625 1630
 Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu
 1635 1640 1645
 50 Leu Leu Glu Thr Ser Trp Glu Ala Leu Glu Arg Ala Gly Ile Asp Pro
 1650 1655 1660
 Ala Arg Leu Arg Gly Ser Arg Thr Gly Val Phe Val Gly Thr Asn Gly
 1665 1670 1675 1680
 55 Gln His Tyr Met Pro Leu Leu Gln Asn Gly Gly Asp Ser Phe Asp Gly
 1685 1690 1695

Tyr Leu Gly Thr Gly Asn Ser Ala Ser Val Met Ser Gly Arg Leu Ser
 1700 1705 1710
 5 Tyr Val Phe Gly Leu Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys
 1715 1720 1725
 Ser Ala Ser Leu Val Ala Leu His Leu Ala Val Gln Ala Met Arg Arg
 1730 1735 1740
 10 Gly Glu Cys Asp Met Ala Leu Val Gly Gly Ala Thr Val Met Ser Thr
 1745 1750 1755 1760
 Pro Glu Met Leu Val Glu Phe Ser Arg Gln Arg Val Ile Ser Ala Asn
 1765 1770 1775
 15 Gly Arg Ser Arg Ala Phe Ala Ala Gly Ala Asp Gly Val Ala Leu Gly
 1780 1785 1790
 Glu Gly Val Gly Val Leu Leu Val Glu Arg Leu Ser Asp Ala Glu Arg
 20 1795 1800 1805
 Asn Gly His Pro Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln
 1810 1815 1820
 25 Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ser Gln Gln
 1825 1830 1835 1840
 Arg Val Ile Arg Gln Ala Leu Ala Asp Ala Gly Leu Arg Pro Glu Asp
 1845 1850 1855
 30 Ile Asp Ala Val Glu Ala His Gly Thr Gly Thr Glu Leu Gly Asp Pro
 1860 1865 1870
 Ile Glu Ala Glu Ala Leu Leu Ala Thr Tyr Gly Arg Thr Arg Thr Ala
 1875 1880 1885
 35 Asp Arg Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Thr
 1890 1895 1900
 Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Leu
 40 1905 1910 1915 1920
 Gly Asn Glu Thr Leu Pro Arg Thr Leu His Val Asp Glu Pro Thr Pro
 1925 1930 1935
 Arg Val Asp Trp Ser Ser Gly Ala Val Ser Leu Leu Thr Glu Pro Val
 45 1940 1945 1950
 Asp Trp Pro Ala Gly Pro Ser Ala Pro Arg Arg Ala Ala Val Ser Ser
 1955 1960 1965
 Phe Gly Ile Ser Gly Thr Asn Ala His Thr Ile Leu Glu Gln Ala Pro
 50 1970 1975 1980
 Val Pro Ala Glu Ser Arg Pro Gly Thr Glu Pro Ala Asp Gly Thr Gly
 1985 1990 1995 2000
 55 Ala Trp Glu Asn Val Thr Val Pro Leu Leu Leu Ser Gly His Thr Glu
 2005 2010 2015

Ala Ala Leu Arg Glu Gln Ser Thr Arg Leu Leu Asn Asp Leu Leu Glu
 2020 2025 2030

5 His Pro Asp Glu His Pro Ala Asp Val Gly Tyr Thr Leu Ile Thr Gly
 2035 2040 2045

Arg Ala His Phe Gly His Arg Ala Ala Val Ile Gly Glu Ser Arg Glu
 2050 2055 2060

10 Glu Leu Leu Asp Ala Leu Lys Ala Leu Ala Glu Gly Arg Glu His His
 2065 2070 2075 2080

Thr Val Val Arg Gly Asp Gly Thr Ala His Pro Asp Arg Arg Val Val
 2085 2090 2095

15 Phe Val Phe Pro Gly Gln Gly Ser Gln Trp Pro Ser Met Ala Arg Asp
 2100 2105 2110

20 Leu Leu Asp Arg Ala Pro Ala Phe Arg Glu Thr Ala Lys Ala Cys Asp
 2115 2120 2125

Ala Ala Leu Ser Val His Leu Asp Trp Ser Val Leu Asp Val Leu Gln
 2130 2135 2140

25 Glu Lys Pro Asp Ala Pro Pro Leu Ser Arg Val Asp Val Val Gln Pro
 2145 2150 2155 2160

Val Leu Phe Thr Met Met Leu Ser Leu Ala Ala Cys Trp Arg Asp Leu
 2165 2170 2175

30 Gly Val His Pro Ala Ala Val Val Gly His Ser Gln Gly Glu Ile Ala
 2180 2185 2190

Ala Ala Cys Val Ala Gly Ala Leu Ser Leu Glu Asp Ala Ala Arg Ile
 2195 2200 2205

35 Val Ala Leu Arg Ser Arg Ala Trp Leu Thr Leu Ala Gly Lys Gly Gly
 2210 2215 2220

Met Ala Ala Val Ser Leu Pro Glu Ala Arg Leu Arg Glu Arg Ile Glu
 2225 2230 2235 2240

40 Arg Phe Gly Gln Arg Leu Ser Val Ala Ala Val Asn Ser Pro Gly Thr
 2245 2250 2255

Ala Ala Val Ala Gly Asp Val Asp Ala Leu Arg Glu Leu Leu Ala Glu
 45 2260 2265 2270

Leu Thr Ala Glu Gly Ile Arg Ala Lys Pro Ile Pro Gly Val Asp Thr
 2275 2280 2285

50 Ala Gly His Ser Ala Gln Val Asp Gly Leu Lys Glu His Leu Phe Glu
 2290 2295 2300

Val Leu Ala Pro Val Ser Pro Arg Ser Ser Asp Ile Pro Phe Tyr Ser
 2305 2310 2315 2320

55 Thr Val Thr Gly Ala Pro Leu Asp Thr Glu Arg Leu Asp Ala Gly Tyr
 2325 2330 2335

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Trp Tyr Arg Asn Met Arg Glu Pro Val Glu Phe Glu Lys Ala Val Arg
 2340 2345 2350

5 Ala Leu Ile Ala Asp Gly Tyr Asp Leu Phe Leu Glu Cys Asn Pro His
 2355 2360 2365

Pro Met Leu Ala Met Ser Leu Asp Glu Thr Leu Thr Asp Ser Gly Gly
 2370 2375 2380

10 His Gly Thr Val Met His Thr Leu Arg Arg Gln Lys Gly Ser Ala Lys
 2385 2390 2395 2400

Asp Phe Gly Met Ala Leu Cys Leu Ala Tyr Val Asn Gly Leu Glu Ile
 2405 2410 2415

15 Asp Gly Glu Ala Leu Phe Gly Pro Asp Ser Arg Arg Val Asn Pro Pro
 2420 2425 2430

Thr Tyr Pro Phe Gln Arg Glu Arg Tyr Trp Tyr His Pro Thr Ser Gly
 2435 2440 2445

20 Arg Arg Gly Asp Ile Thr Ala Ala Gly Val Ala Glu Ala Glu His Pro
 2450 2455 2460

25 Leu Leu Gly Ala Gly Val Glu Leu Pro Glu Thr Gly Gly Thr Val Tyr
 2465 2470 2475 2480

Thr Ala Arg Phe Gly Pro Asp Ser Arg Pro Trp Leu Ala Asp His Ala
 2485 2490 2495

30 Leu Leu Gly Thr Val Leu Leu Pro Gly Thr Ala Ile Leu Asp Leu Val
 2500 2505 2510

Leu Trp Ala Gly Glu Arg Ser Gly Cys Gly Arg Val Gly Glu Leu Ala
 2515 2520 2525

35 Leu Gln Ala Pro Leu Val Leu Pro Asp Ser Gly Asp Val Glu Leu Arg
 2530 2535 2540

Leu Leu Val Gly Pro Asp Glu Glu Lys Arg Arg Thr Val Thr Val
 2545 2550 2555 2560

40 His Ala Arg Pro Ala Ala Ala Gly Ala Glu Ala Pro Trp Thr Arg His
 2565 2570 2575

Ala Glu Ala Val Val Leu Pro Ala Thr Gly Glu Glu Pro Thr Pro Ala
 45 2580 2585 2590

Pro Arg Pro Val Pro Glu Pro Ala Gly Thr Thr Asp Pro Ala Ala Phe
 2595 2600 2605

Tyr Ala Glu Phe Ala Glu Arg Gly Tyr Asp Tyr Gly Pro Ala Phe Gln
 50 2610 2615 2620

Gly Phe Thr Ala Gly Ala Arg His Gly Glu Asp Val Val Ala Glu Val
 2625 2630 2635 2640

55 Ala Leu Pro Ser Gly Leu Val Ala Asp Ala Arg His His Arg Leu His
 2645 2650 2655

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Pro Ala Leu Leu Asp Ala Ala Leu Gln Ala Met Ile Leu Gly Thr Phe
 2660 2665 2670
 5 Phe Ala Asp Asp Gly Arg Ala Arg Met Pro Phe Ala Val Arg Gly Val
 2675 2680 2685
 Arg Leu His Thr Ala Gly Ala Asp Arg Leu Arg Val Leu Ile Ser Pro
 2690 2695 2700
 10 Ala Gly Asp Glu Thr Val Arg Leu Leu Cys Thr Asp Leu Ala Thr Gly
 2705 2710 2715 2720
 Ala Pro Val Leu Glu Ile Asp Glu Leu Val Val Arg Pro Val Ser Gly
 2725 2730 2735
 15 Glu Gln Leu Ala Ala Gly Ala Pro Gly Arg Asn Gly Gly Glu Leu Tyr
 2740 2745 2750
 Arg Val Asp Trp Thr Val Leu Pro Glu Pro Ala Glu Val Pro Ala Pro
 20 2755 2760 2765
 Arg Trp Ala Leu Leu Gly Glu Asp His Ala Gly Leu Ala Asp Val Leu
 2770 2775 2780
 25 Gly Gly Thr Gly Gly Cys Glu Arg Tyr Asp Thr Leu Thr Gly Leu
 2785 2790 2795 2800
 Leu Glu Ala Thr Thr Arg Ser Ala Gly Gly Ile Leu Pro Asp Ile Val
 2805 2810 2815
 30 Ala Leu Ser Leu Pro Thr Ala Pro Glu Pro Gly Pro Gln Ala Val Arg
 2820 2825 2830
 Glu Val Leu Ser Gln Ala Leu Asp Ala Ala Gln Ala Trp Leu Ala Ala
 2835 2840 2845
 35 Gly Ala Glu Thr Ala Ser Ala Arg Leu Val Phe Val Thr Gly Gly Ala
 2850 2855 2860
 Val Ala Thr Thr Ala Asp Glu Thr Val Arg Asp Ile Ala Ala Ala Ala
 2865 2870 2875 2880
 40 Val Trp Gly Leu Val Arg Ser Ala Gln Ser Glu Glu Pro Asp Arg Met
 2885 2890 2895
 Val Leu Leu Asp Leu Asp Gly Glu Arg Pro Thr Ala Arg Thr Leu Ala
 45 2900 2905 2910
 Ala Ala Leu Ala Ser Gly Glu Pro Gln Leu Ala Val Arg Gly Ser Thr
 2915 2920 2925
 Val Ala Ala Pro Arg Leu Ala Pro Ala Gly Pro Gly Pro Glu Asp Leu
 50 2930 2935 2940
 Val Pro Pro Ala Gly Thr Thr Ala Trp Arg Leu Thr Pro Gly Gly Gly
 2945 2950 2955 2960
 Thr Leu Glu Glu Leu Ser Leu Ala Pro Ala Pro Asp Ala Glu Glu Pro
 55 2965 2970 2975

Leu Ala Pro Gly Gln Val Arg Ile Ala Val Arg Ala Ala Gly Val Asn
 2980 2985 2990
 5 Phe Arg Asp Ala Leu Ile Ala Leu Gly Met Tyr Pro Gly Lys Gly Thr
 2995 3000 3005
 Met Gly Ala Glu Gly Ala Gly Val Val Val Glu Thr Ala Pro Asp Val
 3010 3015 3020
 10 Thr Gly Leu Ser Ala Gly Asp Arg Val Leu Gly Met Trp Asn Gly Gly
 3025 3030 3035 3040
 Phe Gly Pro Leu Val Val Ala Asp His Arg Met Val Ala Pro Ile Pro
 3045 3050 3055
 15 His Gly Trp Ser Tyr Ala Glu Ala Ala Ser Val Pro Ala Val Leu Leu
 3060 3065 3070
 Thr Ser Tyr Tyr Ala Leu Thr Arg Leu Ala Arg Ala Arg Thr Gly Gln
 20 3075 3080 3085
 Thr Val Leu Val His Ala Ala Ala Gly Gly Val Gly Met Ala Thr Leu
 3090 3095 3100
 25 Gln Leu Ala Arg His Leu Gly Leu Glu Val Tyr Ala Thr Ala Ser Thr
 3105 3110 3115 3120
 Gly Lys Trp Asp Ala Leu Gln Lys His Gly Ile Pro Asp Asp Arg Ile
 3125 3130 3135
 30 Ala Asp Ser Arg Thr Leu Asp Phe Ala Glu Arg Phe Leu Ser Arg Thr
 3140 3145 3150
 Gly Gly Arg Gly Val Asp Ile Val Leu Asn Ser Leu Ala Gly Glu Phe
 3155 3160 3165
 35 Val Asp Ala Ser Leu Arg Leu Leu Pro Arg Gly Gly His Phe Leu Glu
 3170 3175 3180
 Leu Gly Lys Ala Asp Val Arg Asp Pro Arg Arg Ile Ala Ala Ala His
 3185 3190 3195 3200
 40 Pro Gly Thr Asp Tyr Arg Ala Phe Asp Leu Val Gln Ala Gly Pro Asp
 3205 3210 3215
 Thr Val Gly Glu Met Leu Gly Glu Leu Leu Glu Leu Phe Ala Ala Gly
 45 3220 3225 3230
 Ala Leu Arg Pro Leu Pro Leu Thr Ala Tyr Gly Ile Arg Asp Ala Arg
 3235 3240 3245
 Thr Ala Leu Arg Thr Leu Ser Gln Ala Arg His Thr Gly Lys Leu Val
 50 3250 3255 3260
 Leu Thr Val Pro Ala Gly Phe Asp Thr His Arg Thr Val Leu Leu Thr
 3265 3270 3275 3280
 55 Gly Gly Thr Gly Thr Leu Gly Gln Thr Leu Ala Arg His Leu Val Asn
 3285 3290 3295

Arg His Gly Val Arg His Leu Leu Leu Ala Gly Arg Thr Gly Ala Ala
 3300 3305 3310
 5 Ala Glu Gly Val Ala Glu Leu Ile Gly Glu Leu Gly Glu Leu Gly Ala
 3315 3320 3325
 Glu Val Arg Val Ala Ala Cys Asp Ala Ala Asp Arg Gln Arg Leu Thr
 3330 3335 3340
 10 Glu Leu Leu Ala Gly Ile Pro Val Glu His Pro Leu Gly Ala Val Val
 3345 3350 3355 3360
 His Ala Ala Gly Thr Leu Asp Asp Gly Thr Ile Pro Ser Leu Thr Gly
 3365 3370 3375
 15 Glu Asn Ile Asp Asn Val Leu Arg Pro Lys Ala Asp Ala Val Leu Asn
 3380 3385 3390
 Leu His Glu Leu Thr Arg Asp Ala Asp Leu Ser Ala Phe Val Leu Tyr
 20 3395 3400 3405
 Ser Ser Ser Ser Ala Leu Leu Gly Ser Pro Gly Gln Gly Ala Tyr Ala
 3410 3415 3420
 Ala Ala Asn Ala Phe Leu Asp Gly Phe Ala Arg Tyr Arg Lys Gly Leu
 25 3425 3430 3435 3440
 Gly Leu Pro Ala Leu Ser Leu Ala Trp Gly Leu Trp Gly Ser Asn Ser
 3445 3450 3455
 Arg Met Ala Gly His Leu Asp Gln Ser Gly Met Gln Arg Arg Leu Asn
 30 3460 3465 3470
 Arg Ser Gly Ile Met Ala Leu Thr Asp Ala Glu Gly Leu Ala Leu Phe
 3475 3480 3485
 35 Asp Ala Ala Gln Asp Gly Gly Asp Ala Leu Leu Val Pro Met Arg Leu
 3490 3495 3500
 Asn Arg Thr Ala Leu Arg Ala Ser Gly Arg Ile Thr Pro Phe Leu Ser
 3505 3510 3515 3520
 40 Gly Leu Ala Gly Gly Pro Ala Ala Gly Glu Arg Arg Pro Glu Val
 3525 3530 3535
 Ala Ala Val Ser Gly Thr Leu Ala Glu Arg Leu Thr Gly Leu Thr Ala
 45 3540 3545 3550
 Gln Glu Gly His Ala Leu Val Leu Ala Glu Ile Arg Ala His Ala Ala
 3555 3560 3565
 Ala Val Leu Gly His Gly Ser Asp Asp Ser Ile Pro Glu Asp Arg Ala
 50 3570 3575 3580
 Phe Lys Asp Leu Gly Phe Asp Ser Leu Thr Ala Val Glu Met Arg Asn
 3585 3590 3595 3600
 55 Arg Leu Ser Ala Ala Thr Gly Leu Arg Leu Pro Ala Thr Leu Val Phe
 3605 3610 3615

Asp His Pro Thr Pro Gly Glu Leu Ala Gly His Leu Ser Ala Glu Leu
 3620 3625 3630

5 Ser Ala Asp Asp Ala Pro Gly Ser Ala Ser Pro Leu Thr Glu Leu Asp
 3635 3640 3645

Arg Phe Glu Ala Leu Phe Thr Ala Leu Ala Pro Gly Thr Thr Lys Asp
 3650 3655 3660

10 Thr Pro Gly Gly Ala Gly Ala Leu Met Ile Asp Glu Ala Glu Arg Gln
 3665 3670 3675 3680

Glu Ile Ala Gly Arg Leu Ala Ala Leu Ala Gly Leu Trp Asn Arg Leu
 3685 3690 3695

15 His Gly Thr Thr Ala Pro Glu Asp Gly Asp Thr Val Ala Asp Ala
 3700 3705 3710

20 Leu Glu Ala Ala Asp Asp His Glu Ile Phe Ala Phe Leu Asp Glu Arg
 3715 3720 3725

Phe *
 3730

25 (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1612 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

35 Met Ala Asn Ala Asn Glu Gln Gln Leu Arg Ala Tyr Leu Lys Arg Ala
 1 5 10 15

Thr Thr Glu Leu His Arg Thr Ser Glu Gln Leu Arg Glu Glu Arg Ala
 20 25 30

40 Arg Ala His Glu Pro Ile Ala Val Val Gly Met Ala Cys Arg Tyr Pro
 35 40 45

Gly Gly Ala Asn Thr Pro Glu Gln Phe Trp Glu Leu Leu Asp Thr Gly
 50 55 60

Thr Asp Ala Ala Ala Pro Met Pro Ser Asp Arg Gly Trp Asp Thr His
 65 70 75 80

Gly Leu Tyr Asp Pro Asp Pro Ala Ala Ala Gly Arg Thr Tyr Cys Arg
 85 90 95

Glu Gly Gly Phe Leu His Asp Ala Gly Asp Phe Asp Ala Asp Phe Phe
 100 105 110

55 Gly Ile Ser Pro Arg Glu Ala Val Ala Met Asp Pro Gln Gln Arg Leu
 115 120 125

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Leu Leu Glu Thr Ser Trp Glu Ala Ile Glu Ala Ala Gly Ile Asp Pro
 130 135 140
 5 Arg Gly Leu Arg Gly Ser Arg Thr Gly Val Tyr Val Gly Ala Trp Asp
 145 150 155 160
 Ser Gly Tyr Thr Gly Gln Ala His Ala Pro Ser Ala Glu Leu Glu Ala
 165 170 175
 10 Asp Leu Leu Thr Gly Gly Val Val Ser Phe Thr Ser Gly Arg Ile Ala
 180 185 190
 Tyr Thr Leu Gly Leu Glu Gly Pro Ala Leu Thr Val Asp Thr Ala Cys
 195 200 205
 15 Ser Ser Ser Leu Val Ala Leu His Asn Ala Ala Gln Ala Leu Arg Arg
 210 215 220
 Gly Glu Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met Ala Thr
 225 230 235 240
 20 Pro Ala Val Phe Val Gln Phe Ala Arg Gln Arg Gly Leu Ala Pro Asp
 245 250 255
 Gly Arg Cys Lys Ala Phe Ala Asp Ala Ala Asp Gly Phe Gly Pro Ala
 260 265 270
 Glu Gly Val Gly Met Val Leu Val Glu Arg Leu Ser Asp Ala Arg Arg
 275 280 285
 30 Leu Gly His Pro Val Leu Ala Val Val Cys Gly Ser Ala Val Asn Gln
 290 295 300
 Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ser Gln Glu
 305 310 315 320
 35 Arg Val Ile Arg Gln Ala Leu Gly Asn Ala Arg Leu Thr Val Ala Asp
 325 330 335
 Val Asp Val Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp Pro
 340 345 350
 40 Ile Glu Ala Gln Ala Leu Leu Gly Thr Tyr Gly Arg Asp Arg Asp Gly
 355 360 365
 Gly Arg Pro Val Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala
 370 375 380
 45 Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Met
 385 390 395 400
 Arg Tyr Gly Trp Leu Pro Arg Thr Leu His Val Asp Glu Pro Ser Arg
 405 410 415
 His Val Asp Trp Ser Ala Gly Gly Val Arg Leu Leu Thr Glu Ala Arg
 420 425 430
 50 Glu Trp Pro Gly Val Asp Arg Pro Arg Arg Ala Ala Val Ser Ala Phe
 435 440 445

EP 0 791 655 A2

Gly Val Ser Gly Thr Asn Ala His Leu Ile Leu Glu Ala Pro Asp Thr
 450 455 460
 5 Ala Glu Ala Glu Ser Ala Thr Thr Pro Val Arg Ser Glu Val Ser Glu
 465 470 475 480
 Ser Ala Ala Val Leu Asp Ala Arg Ser Gly Val Val Pro Val Val Val
 485 490 495
 10 Ser Gly Arg Ser Arg Val Val Val Arg Glu Ala Ala Gly Arg Leu Ala
 500 505 510
 Glu Val Val Glu Ala Gly Gly Val Gly Leu Ala Asp Val Ala Val Thr
 515 520 525
 15 Met Ala Gly Arg Ser Arg Phe Gly Tyr Arg Ala Val Val Leu Ala Arg
 530 535 540
 Gly Glu Ala Glu Leu Ala Gly Arg Leu Arg Ala Leu Ala Gly Gly Asp
 20 545 550 555 560
 Pro Asp Ala Gly Val Val Thr Gly Ala Val Val Asp Pro Glu Thr Gly
 565 570 575
 25 Ser Gly Gly Gly Val Val Leu Val Phe Pro Gly Gln Gly Thr Gln
 580 585 590
 Trp Val Gly Met Gly Ala Gly Leu Leu Gly Ser Ser Glu Val Phe Ala
 595 600 605
 30 Ala Ser Met Arg Glu Cys Ala Arg Ala Leu Ser Val His Val Gly Trp
 610 615 620
 Asp Leu Leu Glu Val Val Ser Gly Gly Ala Gly Leu Glu Arg Val Asp
 625 630 635 640
 35 Val Val Gln Pro Val Thr Trp Ala Val Met Val Ser Leu Ala Arg Tyr
 645 650 655
 Trp Gln Ala Met Gly Val Asp Val Ala Ala Val Val Gly His Ser Gln
 660 665 670
 40 Gly Glu Ile Ala Ala Ala Thr Val Ala Gly Ala Leu Ser Leu Glu Asp
 675 680 685
 Ala Ala Ala Val Val Ala Leu Arg Ala Gly Leu Ile Gly Arg Tyr Leu
 45 690 695 700
 Ala Gly Arg Gly Ala Met Ala Ala Val Pro Leu Pro Ala Gly Glu Val
 705 710 715 720
 50 Glu Ala Gly Leu Ala Lys Trp Pro Gly Val Glu Val Ala Ala Val Asn
 725 730 735
 Gly Pro Ala Ser Thr Val Val Ser Gly Asp Arg Arg Ala Val Ala Gly
 740 745 750
 55 Tyr Val Ala Val Cys Gln Ala Glu Gly Val Gln Ala Arg Leu Ile Pro
 755 760 765

Val Asp Tyr Ala Ser His Ser Arg His Val Glu Asp Leu Lys Gly Glu
 770 775 780
 5 Leu Glu Arg Val Leu Ser Gly Ile Arg Pro Arg Ser Pro Arg Val Pro
 785 790 795 800
 Val Cys Ser Thr Val Ala Gly Glu Gln Pro Gly Glu Pro Val Phe Asp
 805 810 815
 10 Ala Gly Tyr Trp Phe Arg Asn Leu Arg Asn Arg Val Glu Phe Ser Ala
 820 825 830
 Val Val Gly Gly Leu Leu Glu Glu Gly His Arg Arg Phe Ile Glu Val
 835 840 845
 15 Ser Ala His Pro Val Leu Val His Ala Ile Glu Gln Thr Ala Glu Ala
 850 855 860
 Ala Asp Arg Ser Val His Ala Thr Gly Thr Leu Arg Arg Gln Asp Asp
 20 865 870 875 880
 Ser Pro His Arg Leu Leu Thr Ser Thr Ala Glu Ala Trp Ala His Gly
 885 890 895
 25 Ala Thr Leu Thr Trp Asp Pro Ala Leu Pro Pro Gly His Leu Thr Thr
 900 905 910
 Leu Pro Thr Tyr Pro Phe Asn His His His Tyr Trp Leu Asp Thr Thr
 915 920 925
 30 Pro Thr Thr Pro Ala Thr Thr Thr Gln Ser Pro Thr Asp Ala Trp Arg
 930 935 940
 Tyr Arg Val Thr Trp Lys Ala Leu Thr Glu Glu Ser Thr Pro Ala Ser
 945 950 955 960
 35 Ser Pro Ser Gly His Trp Leu Leu Val Thr Pro Pro Thr Pro Glu Gly
 965 970 975
 Arg Thr Leu Gly Asp Arg Ala Ala Gly Ala Leu Ala Arg Gln Gly Ala
 980 985 990
 40 Thr Val Glu Arg Leu Val Val Asp Pro Val Ala Val Gly Arg Asp Gly
 995 1000 1005
 Leu Ala Ala Arg Leu Gly Glu Arg Trp Asp Gly Val Leu Ser Leu Leu
 45 1010 1015 1020
 Gly Ala Asp Glu Arg Pro Leu Pro Arg His Pro Ala Leu Asn Arg Ala
 1025 1030 1035 1040
 50 Val Met Gly Thr Thr Leu Leu Ala Gln Ala Ala Leu Asp Ala Gly Cys
 1045 1050 1055
 Glu Ala Arg Ile Trp Ala Val Thr Arg Glu Ala Val Ala Val Ser Pro
 1060 1065 1070
 55 Ser Glu Val Pro Arg Asp Ala Gly Ala Gln Leu Trp Gly Leu Gly Arg
 1075 1080 1085

Gly Ile Ala Leu Glu His Pro Ser Leu Trp Gly Gly Leu Ile Asp Leu
 1090 1095 1100
 5 Pro Ala Val Pro Asp Glu Arg Ala Trp Ala Arg Ala Val Arg Arg Leu
 1105 1110 1115 1120
 Val Pro His Gly Glu Asp Gln Ile Ala Ala Arg Ala Ser Gly Ala Tyr
 1125 1130 1135
 10 Gly Arg Arg Leu Leu Pro Ala Pro Pro Ala Ala Ser Arg Arg Thr Cys
 1140 1145 1150
 Thr Pro Ser Gly Thr Val Leu Val Thr Gly Gly Thr Gly Ala Leu Gly
 1155 1160 1165
 15 Gly His Leu Ala Arg Arg Leu Ala Arg Gly Gly Thr Gly His Leu Val
 1170 1175 1180
 Leu Thr Ser Arg Arg Gly Pro Asp Ala Pro Gly Ala Gly Glu Leu Ala
 20 1185 1190 1195 1200
 Gly Glu Leu Ala Ser Leu Gly Ala Lys Val Thr Val Ala Ala Cys Asp
 1205 1210 1215
 Met Ala Asp Arg Glu Ala Val Arg Ala Leu Leu Asp Glu His Arg Pro
 25 1220 1225 1230
 Thr Ala Val Phe His Thr Ala Gly Thr Pro His Ser Ala Glu Phe Thr
 1235 1240 1245
 30 Ala Leu Asp Glu Thr Thr Ala Gly Val Tyr Gly Gly Lys Val Leu
 1250 1255 1260
 Gly Ala Arg His Leu Asp Glu Leu Thr Arg Glu Leu Gly Ile Gly Leu
 1265 1270 1275 1280
 35 Asp Ala Phe Val Leu Phe Ser Ser Gly Ala Ala Val Trp Gly Ser Gly
 1285 1290 1295
 Gly Gln Thr Ala Tyr Gly Ala Ala Asn Ala Ala Leu Asp Ala Leu Ala
 40 1300 1305 1310
 Glu Arg Arg Ala Ala Gly Leu Pro Ala Thr Ser Val Ala Trp Gly
 1315 1320 1325
 45 Leu Trp Gly Gly Gly Met Gly Glu Gly Asp Gly Glu Glu Phe Leu
 1330 1335 1340
 Ser Arg Arg Gly Leu Gly Val Met Pro Pro Glu Asp Ala Leu Glu Ala
 1345 1350 1355 1360
 50 Leu Asp Arg Ala Leu Asp Arg Glu Asp Thr Thr Val Val Val Ala Asp
 1365 1370 1375
 Val Asp Trp Glu Arg Phe Ala Pro Ala Phe Thr Ala Phe Arg Pro Ser
 1380 1385 1390
 55 Ala Leu Ile Ser Arg Leu Val Ser Asp Gly Gly Glu Ala Gly Gly Gln
 1395 1400 1405

Asp Ala Pro Asp Gly Thr Leu Phe Ala Ala Gly Phe Ala Ala Ala Gly
 1410 1415 1420
 5 Pro Leu Glu Arg Gln Glu Met Leu Leu Gly Leu Val Arg Arg His Val
 1425 1430 1435 1440
 Ala Ala Val Leu Gly His Pro Gly Thr Ala Asp Ile Gly Pro Asp Arg
 1445 1450 1455
 10 Ala Phe Lys Glu Leu Gly Phe Ser Ser Val Thr Ala Val Glu Leu Ala
 1460 1465 1470
 Gly Arg Leu Gly Arg Glu Cys Gly Arg Lys Leu Pro Pro Thr Leu Val
 1475 1480 1485
 15 Phe Asp His Pro Thr Ala Ala Ala Val Glu His Leu Ala Glu Leu
 1490 1495 1500
 Leu Thr Pro Pro Ala Gly Pro Ala Ala Gly Pro Arg Glu Glu Ala
 20 1505 1510 1515 1520
 Arg Ala Ala Leu Ala Arg Val Pro Leu Glu Arg Leu Arg Glu Ala Gly
 1525 1530 1535
 25 Leu Leu Asp Ala Leu Leu Arg Leu Ala Ala Asp Glu Ser Gly Ala Thr
 1540 1545 1550
 Thr Pro Arg Thr Ser Ala Ala Ser Gly Ala Pro Arg Gly Arg Glu Glu
 1555 1560 1565
 30 Pro Asp Gly Arg Gly Glu Pro Asp Gly Ser Gly His Arg Glu Ser Pro
 1570 1575 1580
 Asp Ala Ala Gly Gly Ser Asp Ala Leu Asp Asp Leu Asp Gly Asp Ala
 1585 1590 1595 1600
 35 Leu Val Arg Leu Ala Leu Gly Glu Pro Gly Glu *
 1605 1610

(2) INFORMATION FOR SEQ ID NO:6:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1842 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
 45 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
 50 Met Ala Met Ser Ala Glu Arg Leu Thr Glu Ala Leu Arg Thr Ser Leu
 1 5 10 15
 Lys Glu Ala Glu Arg Leu Arg Arg Gln Asn Arg Glu Leu Arg Ala Ala
 20 25 30
 55 Arg Asp Ala Ala Arg Glu Pro Ile Ala Val Val Gly Met Ala Cys Arg
 35 40 45

Tyr Pro Gly Gly Val Thr Gly Pro Glu Glu Leu Trp Glu Leu Val Ala
 50 .55 60

5 Gly Gly Arg Asp Ala Ile Gly Pro Phe Pro Val Asp Arg Gly Trp Asp
 65 70 75 80

Val Ala Ser Val Tyr Asp Pro Asp Pro Glu Ser Lys Gly Thr Thr Tyr
 85 90 95

10 Cys Arg Glu Gly Gly Phe Leu Glu Gly Ala Gly Asp Phe Asp Ala Ala
 100 105 110

15 Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu Val Met Asp Pro Gln Gln
 115 120 125

Arg Leu Leu Leu Glu Val Ser Trp Glu Ala Leu Glu Arg Ala Gly Ile
 130 135 140

20 Asp Pro Ser Ser Leu Arg Gly Ser Arg Gly Gly Val Tyr Val Gly Ala
 145 150 155 160

Ala His Gly Ser Tyr Ala Ser Asp Pro Arg Leu Val Pro Glu Gly Ser
 165 170 175

25 Glu Gly Tyr Leu Leu Thr Gly Ser Ala Asp Ala Val Met Ser Gly Arg
 180 185 190

Ile Ser Tyr Ala Leu Gly Leu Glu Gly Pro Ser Met Thr Val Glu Thr
 195 200 205

30 Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala Val Arg Ala Leu
 210 215 220

Arg His Gly Glu Cys Gly Leu Ala Leu Ala Gly Gly Val Ala Val Met
 225 230 235 240

35 Ala Asp Pro Ala Ala Phe Val Glu Phe Ser Arg Gln Lys Gly Leu Ala
 245 250 255

Ala Asp Gly Arg Cys Lys Ala Phe Ser Ala Ala Ala Asp Gly Thr Gly
 260 265 270

40 Trp Ala Glu Gly Val Gly Val Leu Val Leu Glu Arg Leu Ser Asp Ala
 275 280 285

Arg Arg Ala Gly His Thr Val Leu Gly Leu Val Thr Gly Thr Ala Val
 290 295 300

45 Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ala
 305 310 315 320

50 Gln Gln Arg Val Ile Ala Glu Ala Leu Ala Asp Ala Gly Leu Ser Pro
 325 330 335

Glu Asp Val Asp Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly
 340 345 350

55 Asp Pro Ile Glu Ala Gly Ala Leu Leu Ala Ala Ser Gly Arg Asn Arg
 355 360 365

Ser Gly Asp His Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly
 370 375 380
 5 His Ala Gln Ala Ala Ala Gly Val Gly Gly Val Ile Lys Met Leu Gln
 385 390 395 400
 Ala Leu Arg His Gly Leu Leu Pro Arg Thr Leu His Ala Asp Glu Pro
 10 405 410 415
 10 Thr Pro His Ala Asp Trp Ser Ser Gly Arg Val Arg Leu Leu Thr Ser
 420 425 430
 Glu Val Pro Trp Gln Arg Thr Gly Arg Pro Arg Arg Thr Gly Val Ser
 15 435 440 445
 Ala Phe Gly Val Gly Gly Thr Asn Ala His Val Val Leu Glu Glu Ala
 450 455 460
 Pro Ala Pro Pro Ala Pro Glu Pro Ala Gly Glu Ala Pro Gly Gly Ser
 20 465 470 475 480
 Arg Ala Ala Glu Gly Ala Glu Gly Pro Leu Ala Trp Val Val Ser Gly
 485 490 495
 Arg Asp Glu Pro Ala Leu Arg Ser Gln Ala Arg Arg Leu Arg Asp His
 25 500 505 510
 Leu Ser Arg Thr Pro Gly Ala Arg Pro Arg Asp Ile Ala Phe Ser Leu
 515 520 525
 30 Ala Ala Thr Arg Ala Ala Phe Asp His Arg Ala Val Leu Ile Gly Ser
 530 535 540
 Asp Gly Ala Glu Leu Ala Ala Leu Asp Ala Leu Ala Glu Gly Arg
 35 545 550 555 560
 Asp Gly Pro Ala Val Val Arg Gly Val Arg Asp Arg Asp Gly Arg Met
 565 570 575
 Ala Phe Leu Phe Thr Gly Gln Gly Ser Gln Arg Ala Gly Met Ala His
 40 580 585 590
 Asp Leu His Ala Ala His Thr Phe Phe Ala Ser Ala Leu Asp Glu Val
 595 600 605
 Thr Asp Arg Leu Asp Pro Leu Leu Gly Arg Pro Leu Gly Ala Leu Leu
 45 610 615 620
 Asp Ala Arg Pro Gly Ser Pro Glu Ala Ala Leu Leu Asp Arg Thr Glu
 625 630 635 640
 Tyr Thr Gln Pro Ala Leu Phe Ala Val Glu Val Ala Leu His Arg Leu
 50 645 650 655
 Leu Glu His Trp Gly Met Arg Pro Asp Leu Leu Leu Gly His Ser Val
 660 665 670
 55 Gly Glu Leu Ala Ala Ala His Val Ala Gly Val Leu Asp Leu Asp Asp
 675 680 685

Ala Cys Ala Leu Val Ala Ala Arg Gly Arg Leu Met Gln Arg Leu Pro
 690 695 700
 5 Pro Gly Gly Ala Met Val Ser Val Arg Ala Gly Glu Asp Glu Val Arg
 705 710 715 720
 Ala Leu Leu Ala Gly Arg Glu Asp Ala Val Cys Val Ala Ala Val Asn
 725 730 735
 10 Gly Pro Arg Ser Val Val Ile Ser Gly Ala Glu Glu Ala Val Ala Glu
 740 745 750
 Ala Ala Ala Gln Leu Ala Gly Arg Gly Arg Arg Thr Arg Arg Leu Arg
 755 760 765
 15 Val Ala His Ala Phe His Ser Pro Leu Met Asp Gly Met Leu Ala Gly
 770 775 780
 Phe Arg Glu Val Ala Ala Gly Leu Arg Tyr Arg Glu Pro Glu Leu Thr
 20 785 790 795 800
 Val Val Ser Thr Val Thr Gly Arg Pro Ala Arg Pro Gly Glu Leu Thr
 805 810 815
 Gly Pro Asp Tyr Trp Val Ala Gln Val Arg Glu Pro Val Arg Phe Ala
 25 820 825 830
 Asp Ala Val Arg Thr Ala His Arg Leu Gly Ala Arg Thr Phe Leu Glu
 835 840 845
 30 Thr Gly Pro Asp Gly Val Leu Cys Gly Met Ala Glu Glu Cys Leu Glu
 850 855 860
 Asp Asp Thr Val Ala Leu Leu Pro Ala Ile His Lys Pro Gly Thr Ala
 865 870 875 880
 35 Pro His Gly Pro Ala Ala Pro Gly Ala Leu Arg Ala Ala Ala Ala
 885 890 895
 Tyr Gly Arg Gly Ala Arg Val Asp Trp Ala Gly Met His Ala Asp Gly
 40 900 905 910
 Pro Glu Gly Pro Ala Arg Arg Val Glu Leu Pro Val His Ala Phe Arg
 915 920 925
 His Arg Arg Tyr Trp Leu Ala Pro Gly Arg Ala Ala Asp Thr Asp Asp
 45 930 935 940
 Trp Met Tyr Arg Ile Gly Trp Asp Arg Leu Pro Ala Val Thr Gly Gly
 945 950 955 960
 Ala Arg Thr Ala Gly Arg Trp Leu Val Ile His Pro Asp Ser Pro Arg
 50 965 970 975
 Cys Arg Glu Leu Ser Gly His Ala Glu Arg Ala Leu Arg Ala Ala Gly
 980 985 990
 55 Ala Ser Pro Val Pro Leu Pro Val Asp Ala Pro Ala Ala Asp Arg Ala
 995 1000 1005

Ser Phe Ala Ala Leu Leu Arg Ser Ala Thr Gly Pro Asp Thr Arg Gly
 1010 1015 1020
 5 Asp Thr Ala Ala Pro Val Ala Gly Val Leu Ser Leu Leu Ser Glu Glu
 1025 1030 1035 1040
 Asp Arg Pro His Arg Gln His Ala Pro Val Pro Ala Gly Val Leu Ala
 1045 1050 1055
 10 Thr Leu Ser Leu Met Gln Ala Met Glu Glu Glu Ala Val Glu Ala Arg
 1060 1065 1070
 Val Trp Cys Val Ser Arg Ala Ala Val Ala Ala Asp Arg Glu Arg
 1075 1080 1085
 15 Pro Val Gly Ala Gly Ala Ala Leu Trp Gly Leu Gly Arg Val Ala Ala
 1090 1095 1100
 Leu Glu Arg Pro Thr Arg Trp Gly Gly Leu Val Asp Leu Pro Ala Ser
 20 1105 1110 1115 1120
 Pro Gly Ala Ala His Trp Ala Ala Val Glu Arg Leu Ala Gly Pro
 1125 1130 1135
 25 Glu Asp Gln Ile Ala Val Arg Ala Ser Gly Ser Trp Gly Arg Arg Leu
 1140 1145 1150
 Thr Arg Leu Pro Arg Asp Gly Gly Arg Thr Ala Ala Pro Ala Tyr
 1155 1160 1165
 30 Arg Pro Arg Gly Thr Val Leu Val Thr Gly Gly Thr Gly Ala Leu Gly
 1170 1175 1180
 Gly His Leu Ala Arg Trp Leu Ala Ala Ala Gly Ala Glu His Leu Ala
 1185 1190 1195 1200
 35 Leu Thr Ser Arg Arg Gly Pro Asp Ala Pro Gly Ala Ala Gly Leu Glu
 1205 1210 1215
 Ala Glu Leu Leu Leu Leu Gly Ala Lys Val Thr Phe Ala Ala Cys Asp
 40 1220 1225 1230
 Thr Ala Asp Arg Asp Gly Leu Ala Arg Val Leu Arg Ala Ile Pro Glu
 1235 1240 1245
 45 Asp Thr Pro Leu Thr Ala Val Phe His Ala Ala Gly Val Pro Gln Val
 1250 1255 1260
 Thr Pro Leu Ser Arg Thr Ser Pro Glu His Phe Ala Asp Val Tyr Ala
 1265 1270 1275 1280
 50 Gly Lys Ala Ala Gly Ala Ala His Leu Asp Glu Leu Thr Arg Glu Leu
 1285 1290 1295
 Gly Ala Gly Leu Asp Ala Phe Val Leu Tyr Ser Ser Gly Ala Gly Val
 1300 1305 1310
 55 Trp Gly Ser Ala Gly Gln Gly Ala Tyr Ala Ala Asn Ala Ala Leu
 1315 1320 1325

Asp Ala Leu Ala Arg Arg Arg Ala Ala Asp Gly Leu Pro Ala Thr Ser
 1330 1335 1340
 5 Ile Ala Trp Gly Val Trp Gly Gly Gly Met Gly Ala Asp Glu Ala
 1345 1350 1355 1360
 Gly Ala Glu Tyr Leu Gly Arg Arg Gly Met Arg Pro Met Ala Pro Val
 1365 1370 1375
 10 Ser Ala Leu Arg Ala Met Ala Thr Ala Ile Ala Ser Gly Glu Pro Cys
 1380 1385 1390
 Pro Thr Val Thr His Thr Asp Trp Glu Arg Phe Gly Glu Gly Phe Thr
 1395 1400 1405
 15 Ala Phe Arg Pro Ser Pro Leu Ile Ala Gly Leu Gly Thr Pro Gly Gly
 1410 1415 1420
 Gly Arg Ala Ala Glu Thr Pro Glu Glu Gly Asn Ala Thr Ala Ala Ala
 20 1425 1430 1435 1440
 Asp Leu Thr Ala Leu Pro Pro Ala Glu Leu Arg Thr Ala Leu Arg Glu
 1445 1450 1455
 25 Leu Val Arg Ala Arg Thr Ala Ala Leu Gly Leu Asp Asp Pro Ala
 1460 1465 1470
 Glu Val Ala Glu Gly Glu Arg Phe Pro Ala Met Gly Phe Asp Ser Leu
 1475 1480 1485
 30 Ala Thr Val Arg Leu Arg Arg Gly Leu Ala Ser Ala Thr Gly Leu Asp
 1490 1495 1500
 Leu Pro Pro Asp Leu Leu Phe Asp Arg Asp Thr Pro Ala Ala Leu Ala
 1505 1510 1515 1520
 35 Ala His Leu Ala Glu Leu Leu Ala Thr Ala Arg Asp His Gly Pro Gly
 1525 1530 1535
 Gly Pro Gly Thr Gly Ala Ala Pro Ala Asp Ala Gly Ser Gly Leu Pro
 40 1540 1545 1550
 Ala Leu Tyr Arg Glu Ala Val Arg Thr Gly Arg Ala Ala Glu Met Ala
 1555 1560 1565
 Glu Leu Leu Ala Ala Ala Ser Arg Phe Arg Pro Ala Phe Gly Thr Ala
 45 1570 1575 1580
 Asp Arg Gln Pro Val Ala Leu Val Pro Leu Ala Asp Gly Ala Glu Asp
 1585 1590 1595 1600
 50 Thr Gly Leu Pro Leu Leu Val Gly Cys Ala Gly Thr Ala Val Ala Ser
 1605 1610 1615
 Gly Pro Val Glu Phe Thr Ala Phe Ala Gly Ala Leu Ala Asp Leu Pro
 1620 1625 1630
 55 Ala Ala Ala Pro Met Ala Ala Leu Pro Gln Pro Gly Phe Leu Pro Gly
 1635 1640 1645

Glu Arg Val Pro Ala Thr Pro Glu Ala Leu Phe Glu Ala Gln Ala Glu
 1650 1655 1660
 5 Ala Leu Leu Arg Tyr Ala Ala Gly Arg Pro Phe Val Leu Leu Gly His
 1665 1670 1675 1680
 Ser Ala Gly Ala Asn Met Ala His Ala Leu Thr Arg His Leu Glu Ala
 1685 1690 1695
 10 Asn Gly Gly Pro Ala Gly Leu Val Leu Met Asp Ile Tyr Thr Pro
 1700 1705 1710
 Ala Asp Pro Gly Ala Met Gly Val Trp Arg Asn Asp Met Phe Gln Trp
 1715 1720 1725
 15 Val Trp Arg Arg Ser Asp Ile Pro Pro Asp Asp His Arg Leu Thr Ala
 1730 1735 1740
 Met Gly Ala Tyr His Arg Leu Leu Leu Asp Trp Ser Pro Thr Pro Val
 20 1745 1750 1755 1760
 Arg Ala Pro Val Leu His Leu Arg Ala Ala Glu Pro Met Gly Asp Trp
 1765 1770 1775
 25 Pro Pro Gly Asp Thr Gly Trp Gln Ser His Trp Asp Gly Ala His Thr
 1780 1785 1790
 Thr Ala Gly Ile Pro Gly Asn His Phe Thr Met Met Thr Glu His Ala
 1795 1800 1805
 30 Ser Ala Ala Ala Arg Leu Val His Gly Trp Leu Ala Glu Arg Thr Pro
 1810 1815 1820
 Ser Gly Gln Gly Gly Ser Pro Ser Arg Ala Ala Gly Arg Glu Glu Arg
 35 1825 1830 1835 1840
 Pro *

(2) INFORMATION FOR SEQ ID NO:7:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: DNA (genomic)
- 50 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 350..14002
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 14046..20036
- 55 (ix) FEATURE:
 (A) NAME/KEY: CDS

(B) LOCATION: 20110..31284

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 31329..36071

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 36155..41830

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	GACCGCTCGG GGAGACCTGA CATATTCGTC GCGAAGTGGT TGTCCGCGCC CCGAGGTACT	60
15	GAAATCTTCT CCGCTCGCCC AGGACTCCGC GTGCAGGTCA CCGGAGTGC CGACCGGCCG	120
	GGACGTCGGA GCGCCGACCC TGCGGACCTG GTGCGATGCC GTGTGGTCCC GCATGATCCC	180
20	GCGCCGTCTC CGGTGACGAG AATCGGTGGA CAATCTCCGA ACTTGACACAA ATTGATTGTC	240
	GTTCACCGGC CGTTTCCCTGTC GCCCCGCAGT TCGCCCGCTG TACGCTCGGG AAGATCAAGA	300
	AAAGGCAGAA AAGCCACGGC GTGGTACGGC GAACATATGA GGGATGCAGG TGTCTGGAGA	360
25	ACTCGCGATT TCCCGCAGTG ACGACCGGTC CGACGCCGTT GCGGTGGTCG GAATGGCGTG	420
	CCGGTTTCCC GGCGCCCCCG GAATTGCCGA ATTCTGGAAA CTGCTGACCG ACGGAAGGGA	480
	CGCGATCGGC CGGGACGCCG ACGGCCGCCG GCGCGGCATG ATCGAGGCCG CCGGCGACTT	540
30	CGACGCCGCC TTCTTCGGCA TGTCACCCCG CGAGGCCGCC GAGACCGACC CCCAGCAGCG	600
	CCTGATGCTC GAACTCGGCT GGGAGGCTCT GGAGGACGCC GGCATCGTCC CCGGCTCCCT	660
	GCGCGCGAG GCGGTGGCG TCCTCGTCG GGCCATGCAC GACGACTACG CCACCCCTGCT	720
35	CCACCGCGCC GGCGCGCCCG TCggccccca CACCGCCACC GGCCTCCAGC GGCATGCT	780
	CGCCAACCGG CTCTCCTACG TCCTGGGAC GCGCGGCCCG AGCCTCGCGG TCGACACCGC	840
40	CCAGTCGTCC TCCCTGGTCG CCGTGGCCCT CGCGTGCAGAG AGCCTGCAGG CCGGCACCTC	900
	CCCGCGTCGCC GTCGCCGGGG CGTCAACCT GGTCTCGCC GACGAGGGAA CGGCCGCAT	960
	GGAACGCCTC GGCGCGCTGT CACCCGACGG CGCGTGCAC ACCTTCGACG CCCGTGCCAA	1020
45	CGGCTATGTC CGCGGTGAGG CGGGCGCCGC CGTCGTCCTG AAGCCCCCTCG CGACGCCCT	1080
	GGCCGACGGG GACCCCGTGT ACTGCGTGGT CGTGGCGTC GCGTCGGCA ACGACGGGG	1140
	CGGCCCCGGG CTGACCGCTC CCGACCGCGA GGGACAGGAG CGGGTGCCTCC GGGCGCCCTG	1200
50	CGCCCCAGGCC CGGGTCGACC CGGCCGAGGT CGTGGTCGTC GAACTGCACG GCACGGGAAC	1260
	CCCGGTGGGC GACCCGGTCG AGGCACACCGC CCTCGGCCGCG GTGCACGGCT CGGGTCGGCC	1320
	GGCCGACGAC CCCCTGCTGG TGGGGTCGGT GAAGACCAAC ATCGGCCACC TGGAGGGCGC	1380
55	CGCCGGCATC CGGGGCCCTGG TCAAGGCCGC ACTGTGCCTG CGGGAACGCA CCCTTCCCGG	1440

	CTCGCTGAAC TTTCGCCACCC CCTCTCCGGC CATCCCGCTG GACCAGCTCC GGCTGAAGGT	1500
5	GCAGACCGCT GCCGCCGAGC TGGCGCTCGC CCCGGGGGGC GCACCCCTGC TGGCGGGTGT	1560
	CAGTTCGTTC GGCATCGGTG GCACCAAATG CCATGTGGTC CTGGAACACC TGCCCTCCCG	1620
	GCCCCACCCCG GCCGTCTCCG TCGCCGCCCTC GCTTCCGGAC GTCCCGCCGC TGTTGTTGTC	1680
10	CGCCGCGGTG GAGGGGGGGT TCGGGGGCAGA GGCAGTGCGG TTGGGTGAGT ACGTGGAGCG	1740
	GGTGGGGGGC GATCCGGGGC ATGTGGCTTA TTTCGCTGGCT TCGACGGGGA CTCTTTTCGA	1800
	GCACCGTGCAG GTGGTGGCGT GTGGTGGCG TCGGGAGCTC GTCGCTGCCTC TTGGTGGTT	1860
15	TGCTGCCGGG AGGGTGTCTG CGGGTGTGCG GTCCGGGGGG GCTGTGCCCG GTGGGGTGGG	1920
	GGTGTGTTTC ACGGGTCAAG GTGCGCAGTG GGTGTGTTATG GCGCGTGGGT TGTATGCCGG	1980
	GGGTGGGGTG TTTGGGGAGG TGCTGGATGA GGTGTTGTCG ATGGTGGGGG AGGTGGATGG	2040
20	TCGGTCGTTG CGGGATGTGA TGGTCGGCGA CGTCGACGTG GACGGGGGTG CGGGGGCTGA	2100
	TGCGGGTCCC GGTGGGGGTG CTGGGGTCGG TTCTGGTTCC GGTTCTGTGG GTGGGGTTGTT	2160
25	GGCTCCGGACG GAGTTTGCTC AGCCTGCGTT GTTGTGCGTTG GAGGTGGCGT TGTTCGGGGC	2220
	GTTGGAGGCT CGGGGTGTGG AGGTGTGCGT GGTGTTGGGT CATTGGTGG GGGAGGTGGC	2280
	TGCTGGTAT GTGGCGGGGG TGTTGTCGTT GGGTGATGCC GTGGGGTTGG TGGTGGCGCG	2340
30	GGCTGGGTTG ATGGGTGGGT TGCCGGTGGG TGGGGGGATG TGGTCGGTGG GGGCGTCGGA	2400
	GTCGGTGGTG CGGGGGGTIG TTGAGGGGTT GGGGGAGTGG GTGTGGTTG CGGCGGTGAA	2460
	TGGGCCGGGG TCGGTGGTGT TGTGGGTGA TGTGGGTGTG CTGGAGTCGG TGGTTGCCCTC	2520
35	GCTGATGGGG GATGGGGTGG AGTGGCGCG GTTGGATGTG TCGCATGGGT TTCATTCGGT	2580
	GTTGATGGAG CGGGTGTIGG GGGAGTTCGG GGGGGTTGTG GAGTCGTTGG AGTTGGTCG	2640
	GGTGGGGCCCG GGTGTGGTGG TGGTGTGGGG TGTGTGGGTG GGGGTGGTGG GTTCGGGGGA	2700
40	GTTGGGGAT CGGGGTATT GGGTGGTCA TGGCGGGGAG GCGGTGCGTT TCGCGGATGG	2760
	GGTGGGGGTG GTGGGTGGTC TGGGTGTGGG GACGTTGGTG GAGGTGGTC CGCATGGGT	2820
45	GCTGACGGGG ATGGCGGGTG AGTGCCTGGG GGCCGGTGAT GATGTGGTGG TGGTGCCGGC	2880
	GATGCGGGCCGG GGCGTGCAGG AGCGGGAGGT GTTCGAGGCG GCGCTGGCGA CGGTGGTCAC	2940
	CCGGGACGCCG GCCCTGGACG CCACGGCACT CCACACCCGGG AGCACCGGCC GGCGCATCGA	3000
50	CCTCCCCACC TACCCCTTCC AACGCCGTAC CCACTGGTCG CCCCGCCTGA GCCGGCCGGT	3060
	CACGGCCGAC GCCGGGGGGGG GTGTGACCGC CACCGATGCC GTGGGGCACA GCGTCTCCCC	3120
	GGACCCGGAG AGCACCGAGG GGACGTCCC CAGGGACACG GACGACGAGG CGGACTCGGC	3180
55	GTCACCGGAG CCGATGTCCC CCGAGGATGC CGTCCGCGCTG GTCCGCGAGA GCACCGCGGC	3240

	CGTCCTGGC CACGACGATC CCGGCAGGT CGCGCTCGAC CGCACCTCA CCTCCCAGG	3300
5	CATGGACTCG GTGACCGCGG TCGAGCTGTG CGACCTGCTG AAGGGCGCCT CGGGGCTCCC	3360
	CCTCGCCGCC ACGCTGGTCT ACGACCTGCC CACCCCGCGT GCCGTGCCG AGCACATCGT	3420
	GGAAGCCGCG GGCGGGCCGA AGGACTCGGT TGCCGGTGGG CCCGGAGTGC TCTCGTCGGC	3480
10	CGCGGTAGGG GTGTGGGACG CCCGGGGCGG CAGCCGGAC GACGACGACC CGATGCCAT	3540
	CGTGGGTGTC GGCTGCCGCC TCCCCGGCGG CGTCGACTCG CGCGCCGCTC TCTGGGAGCT	3600
	GCTGGAGTCC GGCGCCGACG CCATCTCGTC CTTCCCCACC GACCGCGGCT GGGACCTCGA	3660
15	CGGGCTGTAC GACCCCGAGC CCGGGACGCC CGGCAAGACC TATGTGCGGG AGGGCGGGTT	3720
	CCTGCACTCG CGGGCCGAGT TCGACGCGGA GTTCTTCGGG ATATCGCCGC GCGAGGCCAC	3780
	GGCCATGGAC CGCGAGCAGC GCTTGCTGCT GGAAGCGTCG TGGGAGGCC CGAGGACGC	3840
20	CGGAGTGCTC CCCGAGTCAC TGCGCGCGG CGACGCCGA GTGTTCTCGG GCGCCACCGC	3900
	ACCGGAGTAC GGGCCGAGGC TTCACGAGGG AGCGGACGGA TACGAGGGGT ACCTGCTCAC	3960
25	CGGCACCAACC GCGAGCGTGG CCTCCGGCCG GATCGCCTAC ACCCTCGGCA CGGGCGGACC	4020
	GGCGCTCACCG GTCGACACCG CGTGCTCTC GTCCCTGGTG GCGCTGCACC TGGCCGTGCA	4080
	GGCGCTGCGC CGGGGCGAGT GCGGGCTGGC TCTGGCGGGC CGCGCCACCG TGATGTGCGG	4140
30	GCCCCGGCATG TTCTGGAGT TCTCGCCGCA CGCGGGCTC GCCCCCGACG GCGCTGCAT	4200
	GCCGTTCTCC CCCGATGCCG ACGGTACGGC CTGGTCCGAG GGTGTGCCG TACTGGCACT	4260
	GGAGCGGCTC TCCGACGCC CGCGTGCAGG ACACCGGGTG CTGGGCGTGG TGCGGGCAG	4320
35	TCCGGTCAAC CAGGACGGTG CCAGCAACCG CCTGACCGCT CCCAACCGCT CGCGCAGGA	4380
	GGCGTCATC CGAGCTGCC CGGCCGACCC CGGCCTCGCG CGGGGTGACG TGGACCGGTC	4440
	GGAGGCGCAC CGTACGGGA CGGGCCTGGG CGATCCGATC GAGGCGAGCG CGCTGCTGGC	4500
40	CACGTACGGG CGTGAGCGGG TGGCGACCC CTTGTGGCTC GGGTCGCTGA AGTCCAACGT	4560
	CGCTCACACC CAGGCCGCCG CGGGGGCCGC GGGTGTGGTC AAGATGCTGC TTGCCCTGGA	4620
45	CGACCGCACG CTGCCGCCGA CACTTCACGC GGACCGGCCG AGCACGCACG TCGACTGGTC	4680
	GTCGGGCACC GTCGCCCTGC TGGCAGAGGC CGGCCGGTGG CCCCCGGCGGT CGGACCGCCC	4740
	CGCCCGGGCG GCTGTGTGCGT CGTTGGGAT CAGTGGACG AACGCCATC TGATCATCGA	4800
50	GGAGGCCCG QAGTGGGTCG AGGACATCGA CGGCCTCGCT GCTCCTGACC CGGGTACCGC	4860
	GGACCGGGCT GCTCCGTGCC CGCTGTGTT GTCCGCGCGG TCGGAGGGGG CGTTGCCGGC	4920
	GCAGGCCGTG CGTTGGGTG AGTACGTGGA CGGGGTGGGT CGGGATCCGC GGGATGTGGC	4980
55	TTATTGCTG GCTTCGACGC GGACTCTTT CGAGCACCGT CGGGTGGTGC CGTGTGGTGG	5040

	GCCTGGGAG CTCGTCGCTG CTCTTGGTGG GTTTGCTGCC	GGGAGGGTGT CTGGGGTGT	5100
5	GCGCTCCCCG CGGGCTGTGC CGGGTGGGT GGGGCTCTTG	TTCACGGTC AGGGTGCAGA	5160
	GTGGTTCGGT ATGGGGCGTG CGTTGTATGC CCCGGTGGG	GTGTTGCGG AGGTGCTGGA	5220
	TCAGGTGTTG TCGATGGTGG GGGAGGTGGA TGCTGGTGC	TTGCGGGATG TGATGTTCGG	5280
10	CGACGTCGAC GTGGACGCGG GTGCCGGGC TGATGCCGGT	GCCGGTGCAGG GTGCTGGGGT	5340
	CGCTTCTGGT TCCGGTTCTG TCCGTGGCTT GTTGGCTCGG	ACGGAGTTTG CTCAGCCTGC	5400
	GCTGTTGCGG TTGGAGGTGG CGTTGTTCCG GCGCTTGGAG	GCTCGGGGTG TGGAGGTGTC	5460
15	GGTGGTGGTG GGTCAATTCCG TCGGGGAGGT GGCTGCTGC	TATGTGGCGG GGGTGGTGT	5520
	GTTCGGTGTAT CGGGTCCGGT TCGTGGTGC GCGGGTGGG	TTGATGGTGC GGTGGCCGGT	5580
	GGCTGGGGGG ATGTGGTCCG TCGGGGCGTC GGAGTCGGTG	GTGCGGGGGG TTGTTGAGGG	5640
20	GTTCGGGGAG TCGGTGTCCG TTGGGGCGGT GAATGGGCCG	CGGTGGTGG TGTTGTCGGG	5700
	TGATGTGGGT GTGCTGGACT CGGTGGTTCG CTCGCTGATG	GGGGATGGGG TCGAGTGCAG	5760
25	GGGGTTGGAT GTGTCGCATG GGTTCATTG GGTGGTGTATG	GAGCCGGTGT TGGGGAGTT	5820
	CGGGGGGGTT GTGGACTCGT TCGAGTTCCG TCGGGTGC	CCGGGTGTGG TGGTGGTGT	5880
	GGGTGTGTGG CGTGGGGTGG TGGGTTCCG GGAGTTGGGG	GATCCGGGT ATTGGGTGCG	5940
30	TCATGCGCGG GAGCCGGTCC GTTTCGGGA TGGGGTGGGG	GTGGTCCGTG GTCTGGGTGT	6000
	GGGGACGTTG GTGGAGGTGG GTCCGCATGG GGTGCTGACG	GGGATGGCGG GTGAGTGCCT	6060
	GGGGGCCGGT GATGATGTGG TCGTGGTGC GCGGATGCAG	CGGGGCCGTG CGGAGCGGGA	6120
35	GGTGGTCCAG GCGGGCGTCG CGACGGTGT CACCCGGAC	GCCGGCCTGG ACCAACCGCC	6180
	ACTCCACACC GGGACCAACCG GCCGGCGCAT CGACCTCCCC	ACCTACCCCT TCCAACGCGA	6240
	CCGCTACTGG CTGGACCCCG TTCGCACCGC CGTGACCGGC	GTCGAGCCCG CGGGCTCGCC	6300
40	GGCGGACGCT CGGGCCACTG AGCGGGGACG GTGACGACG	GCCGGGATCC GCTACCGCGT	6360
	CGCTTGGCAG CGGGCCGTGC TCGACCCGGG CAACCCGGG	CCTGCGGGTC ATGTGCTGCT	6420
45	TCTGGCCCCG GACCGAGGACA CGGCCGACTC CGGACTCGCC	CCCGCGATCG CACGTGAAC	6480
	CGCCGTGCAG GGGGGCGAGG TCCACACCGT CGCCGTGCCG	GTCGGTACAG GCCGGGAGGC	6540
	AGCCGGGGAC CTGGTGGGG CGGCGGGTGA CGGTGCCGCC	CGCAGCACCC GAGTTCTGTG	6600
50	GCTCGCCCCG GCCGAGCCGG ACGGGGCGA CGCCGTGCC	CTCGTCCAGG CGCTGGCGA	6660
	GGCGGTACCC GAAGCCCCC TCTGGATCAC CACCCGTGAG	GGGGCGGGCC TCGGGCCCGA	6720
	CGAGACCCCT TCCGTGGGG CGCCTCAGCT GTGGGGACTC	GGACAGGTGG CGGGCCTCGA	6780
55	ACTGGGGCGG CGCTGGGGCG GCTTGGCGGA CCTGCCCCGGG	AGTGGTGCAG CGGGCGGTGCT	6840

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5	CGCGTCCAT	GTCCGCCGTG	TGGTTCCCGC	GCCC GTCCCC	GTCCCGGCCT	CCGCTCGCAC	6960
	CGTCACCACG	GCCCCCGCCA	CCGCCGT CGG	CGAGGACGCA	CGGAACGACA	CCTCGGACGT	7020
	GGTCGTGCCG	GACGACCGGT	GGTCCTCCGG	CACCGTACTG	ATCACCGGGG	GCACCGGTGC	7080
10	CCTGGGTGCG	CAGGTGCCCC	GCAGGCTCGC	CCGGT CGGGC	GCCGCGCGTC	TGCTCCTGGT	7140
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15	CCTCGGGGC	CTCCCCGAGG	AGCGGGCCCT	CGTCGCCGTA	CTGCACGCGG	CAGGTGTGCT	7320
	CGACGACGGT	GTGCTCGACT	CGCTCACCTC	CGACCGGGTG	GACGCCGTAC	TGCGGGACAA	7380
20	GGTCACCGCC	GCCC GT CACC	TGGACGAGCT	GACCGCGGAC	CTTCGCTCG	ACGCCCTCGT	7440
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25	GATCGCTTGG	GGGCCGTGGG	CCGGT CGGGC	AATGGCCCTCC	GGAACGGCGG	CGAAGTCCCTT	7620
	CGAACGGGAC	GGCGTACGG	CCCTGGACCC	CGAGCGCGCG	CTCGACGTCC	TCGACGACGT	7680
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30	CGTCGCCGAC	GTGGACTGGG	AGACCTTCGT	CGGGCGTTCG	GTCACCCGCC	GTACCTGGTC	7800
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40	GCTCGACCCG	GAGCTGGCCT	TCCGGTCCCG	CGGGTTTCGAC	TCCCTCACCG	TTCTCGAACT	8100
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	GGTGCAGGCGG GCCGCGGTGT CGGCGTTCGG GGTGAGCGGG ACCAACGCCG ATGTGGTCCT	9540
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	TCAGGTCGGC CTCCGACGAC GACTTGTTCG ACCTGCTCGA CAGCGACTTC CAGTGAGCGG	20040
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	GTCATGTACC ACGACTACGG CAGCCACCAAG GTCGGCACCG CCGCCGATCC CAGTGACAG	20640
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	GCCCAGCAGC GGGTGATCCG TGACGGCTG GCGACGCCGG GGCTGACGCC CGCCGACGTG	21120
	GACCGGGTCG AGGCGCACGG CACCGGCACA CGCGTCGGCG ACCCGATCGA GGCGGGCGCG	21180
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	CTGCTCGCGC ACGACGGAGC CCCGGTCGAC GCACTCGCCG CCCTCGCCGC CGCGAGACC	21840
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30	TCGACAGGCT GACCGCGCTG GCGGAGGACA GGAAGGACCC CGCGTCACC GTGGCGAGG	33000
	CGGGCAGCGG CGGGCCCCCCC GTCTTCGTCT TCCCGGGACA GGGCTCCCAG TGGACGGCA	33060
	TGGCGCCGA ACTCCTGGAC AGGGCACCGG TCTTCCGCGC CAAGGCCAG GAGTGCAGCG	33120
35	GGGCCCTCGC GGCCCACCTC GACTGGTCGG TGCTCGACGT CCTGCGCGAC GCGCCGGCG	33180
	CCCCGCCGAT CGACCGCGCG GACGTCGTCC AGCCGACCCCT GTTCACCATG ATGGTCTCCC	33240
	TCGCGCGCT GTGGGAGTCC CACGGTGTAC GGCGCCGCCG CCGGGTCCGC CACTCCAAAG	33300
40	GCGAGATCGC CGCCGCCAC CGGGCCGGTG CCCTGTCCCT CGACGACCGG GCGCGCTGA	33360
	TCGCCGAGCG CAGCAGGCTC TGGAAAGGGC TGGCCGGAAA CGCGGGCATG CTCTCCGTGA	33420
	TGGCCCCGGC CGACCGGGTC CGCGAACTGA TGGAGCCCTG GGCGGAGCGG ATGTCCTGG	33480
45	CCGCCGTCAA CGGCCCCGCC TCGGTACCCG TGGCCGGTGA CGCGCGGGCG CTGGAGGAGT	33540
	TCGGGGGCCG GCTCTCCGCC GCCGGGGTGC TGGCGTGCC CCTCGCCGCC GTCGACTTCG	33600
50	CCGGACACTC ACCCCAGGTG GAGCAGTTCC GCGCCGAGCT CCTCGACACG CTGGCACCG	33660
	TCCGCCGAC CGCCGCCCGG CTGCCCTTCT TCTCCACCGT GACCGCCCG GCGCACGAGC	33720
	CCGAAGGCCT GGACGCCGCG TACTGGTACC GGAACATGCG CGAACCCGTG GAGTCGCGT	33780
55	CCACCCCTGCG GACGCTGCTG CGCGAGGGCC ACCGCACCTT CGTCGAGATG GGCGCGCACC	33840

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5	TCGCCACCCCT CCACCGCGGC TCCGGCGGCC TGGACCGGTT CCGCTCCTCG GTGGCGGCCG	33960
	CGTTCGCCCCA CGGAGTACGG GTCGACTGGG ACGCCCTCTT CGAGGGCTCC GGCGCCCGCC	34020
	GGGTCCCCGT GCCCACCTAC GCCTTCAGCC GGGACCGGTA CTGGCTGCC ACCGCCATCG	34080
10	GCCGGCGCGC CGTCGAGGCG GCCCCCGTCG ACGCGTCCGC CCCCCGGCGC TACCGCGTCA	34140
	CCTGGACACC CGTGGCATCC GACGACTCCG GCCGGCCCTC CGGGCGCTGG CTGCTGGTGC	34200
	AGACCCCCCGG CACCGCGCCG GACGAGGCCG ACACCGCGGC GTCGGCCCTC GGTGCGGCCG	34260
15	GGGTGGTCGT GGAGCGCTGC CTGCTGGATC CCACCGAGGC CGCGCGCGTC ACGCTCACCG	34320
	AGCGACTGGC CGAACCTGGAC GCGCAGCCGG AGGGCCTGGC CGCGTGCTG GTGCTGCCG	34380
	GCCGTCCGCA GAGCACCGCA CCGGCCGACG CCTCCCCGCT CGACCCGGGG ACGGCCGCCG	34440
20	TCCCTGCTCGT GGTCCAGGCC GTGCCCGACG CCGCTCCGAA GGCCCCGATC TGGGTGGTGA	34500
	CGCGGGGTGC GGTGGCGGTG GGGTGGGTG AGGTGCCGTG TGCGGTGGGT GCGCGGGTGT	34560
	GGGGTCTGGG GCGGGTGGCT GCGTTGGAGG TGCCGGTGCA GTGGGGTGGG TTGGTGGATG	34620
25	TGGCGGTGGG GGCGGGTGTG CGTGAGTGGC GTCGTGTGGT CGCTGTGGTT CGGGGGGGTG	34680
	GTGAGGATCA GGTGGCGGTG CGTGGTGGGG GTGTGTTCTGG TCGTCGTCTG GTGGGTGTGG	34740
30	CGGTGCCGGG TGGTICGGGG GTGTGGCGTG CGCGGGGGTG TGTGGTGGTG ACGGGTGGGT	34800
	TGGGTGGTGT GGGGGGTCA GTGGCGCGGT GGTTGGCGCG TTCGGGTGCG GAGCATGTGG	34860
	TCTTGGCCGG GCGTCGGGGT GGTGGGGTTC TGCGGGCGGT GGAGTTGGAG CGGGAGTTGG	34920
35	TGGGGTTGGG GGCGAAGGTG ACGTTCTTT CGTGTGATGT GGGGGATCGG GCGTCGATGG	34980
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	CGGGGGTGGC TCAGGTGTG TGCGGGTGG AGGTGTCTTG GGCGGAGGCC GGTGGTGTGT	35100
40	TGGGGGTAA GGCGGTGGGG GCTGAGTTGT TGGACGAGTT GACGGCGGGT GTGGAGCTGG	35160
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	ATGCCGCGGC CAATGCCAT CTGGATGCCGT TGCGGGAGCG TCGTCGTGCG CAGGGCGTC	35280
45	CCCGCACCTC CGTCGCCTGG GGCCTGTGGG GCGCGAGGG CATGGGAGCG GACGAAGGCC	35340
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50	CACTGCACAC GCCACTGAAC GAGGGCGACA CCTGCCTCAC GGTCGCCAC ATCGACTGGG	35460
	AACACTTCGT CACCGGGTTC ACCGCCTACC GGGCCAGCCC CCTGATCTCC GACATCCCCC	35520
	AGGTCCGCGC GTTGCACG CCCGAACCCA CCGTGGACGC CTGGACCGA CTGGCGCCGGC	35580
55	GGTGCACGC CGCCCTCACC CGCGCGAGC GCACCAAGGT CCTGGTGCAC CTGGTCCGCA	35640

	CGGTGGCGGC GGAGGTCCTC GGTCACGACG GGATCGCGG CATCGGCCAC GACGTGGCCT	35700
5	TCCGGGACCT CGGCTTCGAC TCGCTGGCCG CGGTGCGGAT GCGCGGCCGG CTGGCCGAGG	35760
	CGACCGGACT CGTACTGCCC GCGACGGTCA TCTTCGACCA CCCCACCGTG GACCGGCTCG	35820
	GCGCGCGCT GCTGGAGCGG CTGTCCGCGG ACGAACCCGC GCCCCGGCGG GCGCCGGAGC	35880
10	CCGCCGGGGG GAGGCCCGCG ACCCCACCGC CCGCACCGGA GCCGGCCGTC CACGACGCCG	35940
	ACATCGACGA ACTCGACGCG GACGCCCTGA TCCGGCTGGC CACCGGAACC GCCGGACCGG	36000
	CCGACGGCAC GCCGGCCGAC GGCGGGCCCG ACGCGGCGGC GACCGCCCCC GACGGAGCAC	36060
15	CGGAGCAGTA GCGCGCCCTC ACCGGCGCGC CGACCGGCGG AGCGCCGTAC CGCCGACGCC	36120
	CCCCACAGCC AGCGAGCAGA CGAGGAAGCC GAAGATGTCA CCGTCCATGG ACGAAGTGCT	36180
	GGGTGCGCTG CGCACCTCCG TCAAGGAGAC CGAGCGGCTG CGCCGGCACA ACCGGGAGCT	36240
20	CCTGGCCGGC CGGCACGAGC CGGTGCCCAT CGTGGGCATG GCCTGCGCGT ACCCCGGTGG	36300
	CGTGAGCACC CGGGACGACC TGTGGGAGCT CGCCGCGGAC GGCGTCGACG CGATCACCCC	36360
25	CTTCCCGGCC GACCGGGGCT GGGACGAGGA CGCCGTCTAC TCGCCCGACC CCGACACCCC	36420
	CGGCACCAACC TACTGCCGTG AGGGCCGCTT CCTCACCGGC GCGGGGACT TCGACGCCG	36480
	CTTCTTCGGC ATCTCGCCGA ACGAGGCGCT GGTGATGGAC CCGCAGCAGC GGCTGTTGCT	36540
30	GGAGACGTCG TGGGAGACGT TGGAGCGGGC CGGCATCGTC CCCGCGTCGC TGCGCGGCAG	36600
	CCGTACCGGT GTCTTCGTG GAGCCCGCA CACGGGATAC GTCACCGACA CCGCGCGAGC	36660
	GCCCGAGGGC ACCGAGGGCT ATCTGCTGAC GGGCAACGCC GATGCCGTCA TGTCCGGCCG	36720
35	GATCGCCTAC TCCCTGGGTC TGGAGGGGCC GGCCTGACG ATCGGGACGG CCTGCTCGTC	36780
	GTCGTTGGTG GCGTTGCATC TGGCGGTGCA GTCGTTGCGG CGGGGCGAGT GCGACCTGGC	36840
	GTTGGCCGGC GGCGTCGCGG TCATGCCGA CCCGACGGTG TTCGTGGAGT TCTCGCGCA	36900
40	GCGGGGGCTG CGCGTGGACG GGCGTGCAA GGCCTTCGCG GAGGGTGCAG ACGGGACGGC	36960
	GTGGCCGGAG GGAGTGGGTG TGCTGCTGGT GGAGCGGCTT TCCGACGCGC GCCGCAATGG	37020
45	CCATCGGGTG CTGGCGGTGG TGCGGGCAG TGCGGTCAAT CAGGACGGGG CGAGCAATGG	37080
	GCTGACGGCG CCGAGTGGTC CTGCGCAGCA GCGGGTGATC CGTGAGGCCG TGGCTGATGC	37140
	GGGCGTGACG CCCGCCGACG TGGATGTGGT GGAGGGCGAC GGTACGGGA CGGGCGTTGGG	37200
50	TGATCCGATC GAGGCAGGTG CGTTGCTGGC CACGTACGGG CGGGAGCGGG TCGGTGATCC	37260
	TTTGTGGTTCG GGGTCGTTGA AGTCGAACAT CGGGCATGCG CAGGCGGCTG CGGGTGTGGG	37320
	TGGTGTGATC AAGGTGGTGC AGGCGATGCG GCATGGTGC TTGCGCGGA CGCTGCATGT	37380
55	GGATCGCGCCG TCGTCGAAGG TGGAGTGGGC TTGCGGTGCG GTGGAGCTGC TGACCGAGGG	37440

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	CTCGGCACGC TCGCGGGAGG CGCTGCGCG CCAGGCCGA CGACTCGCCG CTCTCGCCG	37680
10	CCAGGGGCGC ACGGAGGGCA CGGGCGCGG CAGCGGACTC GTCTCCCCG CGGCCGACAT	37740
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	CGCCCAGCGG CTCGGCGCCG GTCGGGAGCT CCGCGGCAGG TTCCCCGTCT TCGCCGACGC	37980
	CCTCGACGAG ATCCCGGGGG AGTTCGACGC CCACCTCGAA CGCCCTCTCC TGTCGGTGAT	38040
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25	GGACGTCTCTC GTGGGCCACT CGATCGGCGG TCTGGTGGCG GCTCACGTGG CGGGCGTCTT	38220
	CTCTCGGGCC GACCGGGCCC GGCTGGTCTC CGCACCGGGC CGGCTCATGC GGGCCCTGCC	38280
	CGAGGGCGGC GCGATGGCGG CGTGCAAGGC CACCGAGCGG GAGGCCGCCG CGCTGGAGCC	38340
30	CGTCGCCGCC CGCGGGCGG TGGTCGCCGC GGTCAACGGC CCGCAGGCC CTCGTGCTCTC	38400
	CGGGGACGAG CGGGCCGTAC TGGCGCGGC CGGTGAAC TG GCCGCCCCG GACGCCGCAC	38460
	CAAGCGCCTG AGGGTGAGCC ACGCCTTCCA CTCACCCCGT ATGGACGCCA TGCTGCCGA	38520
35	CTTCCGGCGG CTGGCGGACA CGGTGACTA CCACGCCCG CGGCTGCCGG TCGTCTCCGA	38580
	AGTGACCGGC GACCTCGCCG ACGCCGCCA GCTGACCGAC CCCGGCTACT GGACCCGCCA	38640
	GGTGGCCAG CGGGTGGCGT TCGCCGACGC CGTGCGCACC GCGAGGCCCG GGGACGCCGC	38700
40	GACCTTCATC GAGCTCGGGC CGGACCCGT CCTGTGCGGC ATGGCGGAGG AGTCCCTGGC	38760
	CGCGGAGGCC GACGTCGTGT TCGCCCCGGC ACTGCGCCGC GGGCGCCCG AGGGCGACAC	38820
45	CGTGTCCGG CGCGCCCGA GCGCTACGT CCGCGGCCG GGCCTCGACT GGGCCCGCGCT	38880
	CTACGGCGGC ACGGGAGCCC GCCGCACCGA CCTGCCACC TACGCCCTCC AGCACAGCCG	38940
	CTACTGGCTC GCCCCCGCCT CGGGCCGGT CGGGCCCGCG ACGGCCGCCCG CCTCCGTCCG	39000
50	ATCCGTGCCG GAAGCCGAGC AGGACGGGGC GCTGTGGGCC GCCGTGCACG CGGGTGACGT	39060
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	GGTCCTGCCG CACCTGGCCG CCTGGCACGA CGCGACCGC GCGACCGCGC GGACCGCGGG	39180
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	CGCACGGAGC CCGGAGGGCC TGGCCGGCGT GCTGCTGCTC CCCGACTCGG GCGGTGCCGC	39480
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	ACTGACCGAC GCCGCGGTGC CGGCACCGCT GTGGGTGGTG ACGCGGGGTG CGGTGGCGGT	39600
	GGGGTCGGGT GAGGTGCCGT GTGCGGTGGG TGCGCGGGTG TGGGGTCTGG GCGGGTGGC	39660
15	TGCGTTGGAG GTGCCGGTGC AGTGGGGTGG GTTGGTGGAT GTGGCGGTGG GGGCGGGTGT	39720
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	GGAGGGGTTG GGGGTGCCGT TGCGTGGTGT GTTTCATGCG GCGGGGGTGG CTCAGGTGTC	40140
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	GTGGGTGCT GGGGTGTGGG GGAGTGGGGG GCACTGGGTG TATGCGGCCG CCAATGCGCA	40320
35	TCTGGATGCG TTGGCGGAGC GTCGTGTGCG GCAGGGCGT CCCGCGACCT CCGTCGCCTG	40380
	GGCCCCGTGG GACGGCGACG GCATGGCGA GATGGCGCCC GAGGGCTACT TCGCCGCCA	40440
	CGGGTGGGCC CCGCTCCACC CCGAGACGGC GCTCACCGCC CTGCACCAGG CCATCGACGG	40500
40	CGGCGAAGCC ACGGTACCG TGGCGGACAT CGACTGGAA CGGTTGCCCC CGGGCTTCAC	40560
	CGCCTTCCGT CCCAGCCCC TGATGCCGG CATCCCCGCG GCGCGTACGG CGCCCGCCGC	40620
45	CGGGCGGGCCC GCCGAGGACA CCCCCACCGC CCCCCGGCTC CTGCGGGCGC GGCCCGAGGA	40680
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50	CGGGGTGCGG CTGCGCCGCC GGCTGGCGA GGACACCGGG CTGACCTGCG CCGGCACCCCT	40860
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	GGGGACCCCCC GGCCCCCAGG AGGGCACGGC TCGGGCCGAG AGCGGGCTGT TCGCCTCCTT	40980
55	CCGGCGCGCC GTCGAACAGC GCAGGTGAG CGAGGTGCGTG GAGCTGATGG CCGACCTGGC	41040

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	CGCCCTTCCC CTGTCCGGCT TCGGGACCC CGCGGAACCG ATGCCCCAT CGCTCGACGC	41280
10	GCTGATCGAG GTCCAGGCCG ACGTCCTCCT GGAGCACACC GCGGGCAAGC CCTTCGCCCT	41340
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	CGGCTCGGGC CCCGCAGCCG TCGTACTGAT GGACGTCTAC CGTCCCGAGG ACCCCGGTGC	41460
15	GATGGGCAGAG TGGCGCGACG ACCTGCTCAG CTGGGCGCTC GAACGCAGCA CGGTGCCCT	41520
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	CGACGTGCCCG GGCAACCACT TCACCATGCT CACCGAACAC GCCC GGACACA CCGCGTCCCT	41760
	GGTGACGAA TGGCTGGACA GCCTCCCGCA CCAGCCCGT CCCGCCGGC TCACCGGAGG	41820
25	GAAACACTGA TGTACGCCGA CGACATCGCG GCCGTCTACG ACCTGGTCCA CGAGGGGAAG	41880
	GGGAAGGACT ACCGGCAGGA GGCGAGGAG ATCGCCGCAC TCGTGCGCGT CCACCGGGCG	41940
30	GGCGCCCGGA CCCTGCTCGA CGTGGCCTGC GGCACCGGCC AGCACCTGCA CCACCTGGAC	42000
	GGCCTCTTCG ACCACGTCGA GGGCCTGGAA CTCTCCGCG ACATGCTGGC CCTCGCGACC	42060
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35	CGGTTGACG CGGTGACCTG CATGTTCAAGC TCCATAGGCC ACCTGGGAC CACCGACGAA	42180
	CTCGACAGCA CGCTGCGGGC CTTCACCGAC CACCTCGAAC CGTCCGGCGT CATCGTCGTC	42240
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45	ACCATCACCC TGTTCGGCG CGCGACTAC GAGGCGGCCT TCGAGCGCGC CGGCTGGAC	42480
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	CCCGGTGCCG ACGCGGACCG CGCGGGCCCG GAGGGGGTT GCCCCGACCC ACCCGGCACA	42600
50	CCCGGGTCCC CCGATCGTGC GAGGCCCCC ATCGACCCGA GAAGAAAGGC AGGGCAGCCA	42660
	TGCCCACCGT ACGGCCCCCG CGAGCACGAG CACGAGCGCG GGCACGAGCA	42720
	CGGGCGTCCG TGCGCTCGGC CGTCGGCTCC AGCTGACCCG GGCGCACAC TGGTGCACCG	42780
55	GCAACCAGGG CGACCCGTAC GCGCTGATCC TGCGCGCCGT CGCCGACCCC GAGCCGTTCG	42840

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10	CGGCCCCAGGC GCCCTGCGCG GCGCGCACCA CCGCCCGCAG AGTGCTCGGC CGCCTGCTGC	43140
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40	CCTCCACCGG TCTGACCGCC GTACGGGTGG GCGACGACCG ACCGGCCGCG GAGCTGCTCG	44160
	CCGAGATGGG CAGAGACCTC GTCCCCTACC AGAGGGCTT CGAGTTGGT GAGGTGGAGA	44220
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45	GCTTCGCCCC GTTCAACGGC GCCGCCACGA TGGACGAGAT CGTCGACTTC GCCCGTGGCT	44340
	GGCGGGCCGA CCTGGTCGTG TGGCAACCCCT GGACCTA	44377

50 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4550 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

	Met Ser Gly Glu Leu Ala Ile Ser Arg Ser Asp Asp Arg Ser Asp Ala	
1	5	10
	Val Ala Val Val Gly Met Ala Cys Arg Phe Pro Gly Ala Pro Gly Ile	
10	20	25
	Ala Glu Phe Trp Lys Leu Leu Thr Asp Gly Arg Asp Ala Ile Gly Arg	
	35	40
15	Asp Ala Asp Gly Arg Arg Gly Met Ile Glu Ala Pro Gly Asp Phe	
	50	55
	Asp Ala Ala Phe Phe Gly Met Ser Pro Arg Glu Ala Ala Glu Thr Asp	
	65	70
20	Pro Gln Gln Arg Leu Met Leu Glu Leu Gly Trp Glu Ala Leu Glu Asp	
	85	90
25	Ala Gly Ile Val Pro Gly Ser Leu Arg Gly Glu Ala Val Gly Val Phe	
	100	105
	Val Gly Ala Met His Asp Asp Tyr Ala Thr Leu Leu His Arg Ala Gly	
	115	120
30	Ala Pro Val Gly Pro His Thr Ala Thr Gly Leu Gln Arg Ala Met Leu	
	130	135
	Ala Asn Arg Leu Ser Tyr Val Leu Gly Thr Arg Gly Pro Ser Leu Ala	
	145	150
	155	160
35	Val Asp Thr Ala Gln Ser Ser Leu Val Ala Val Ala Leu Ala Val	
	165	170
	175	
	Glu Ser Leu Arg Ala Gly Thr Ser Arg Val Ala Val Ala Gly Gly Val	
	180	185
40	190	
	Asn Leu Val Leu Ala Asp Glu Gly Thr Ala Ala Met Glu Arg Leu Gly	
	195	200
	205	
	Ala Leu Ser Pro Asp Gly Arg Cys His Thr Phe Asp Ala Arg Ala Asn	
	210	215
	220	
45	Gly Tyr Val Arg Gly Glu Gly Gly Ala Ala Val Val Leu Lys Pro Leu	
	225	230
	235	
	240	
	Ala Asp Ala Leu Ala Asp Gly Asp Pro Val Tyr Cys Val Val Arg Gly	
	245	250
	255	
50	Val Ala Val Gly Asn Asp Gly Gly Pro Gly Leu Thr Ala Pro Asp	
	260	265
	270	
	Arg Glu Gly Gln Glu Ala Val Leu Arg Ala Ala Cys Ala Gln Ala Arg	
	275	280
	285	
55	Val Asp Pro Ala Glu Val Arg Phe Val Glu Leu His Gly Thr Gly Thr	

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	290	295	300
	Pro Val Gly Asp Pro Val Glu Ala His Ala Leu Gly Ala Val His Gly		
5	305	310	315
	Ser Gly Arg Pro Ala Asp Asp Pro Leu Leu Val Gly Ser Val Lys Thr		
	325	330	335
10	Asn Ile Gly His Leu Glu Gly Ala Ala Gly Ile Ala Gly Leu Val Lys		
	340	345	350
	Ala Ala Leu Cys Leu Arg Glu Arg Thr Leu Pro Gly Ser Leu Asn Phe		
	355	360	365
15	Ala Thr Pro Ser Pro Ala Ile Pro Leu Asp Gln Leu Arg Leu Lys Val		
	370	375	380
	Gln Thr Ala Ala Ala Glu Leu Pro Leu Ala Pro Gly Gly Ala Pro Leu		
	385	390	395
	400		
20	Leu Ala Gly Val Ser Ser Phe Gly Ile Gly Gly Thr Asn Cys His Val		
	405	410	415
	Val Leu Glu His Leu Pro Ser Arg Pro Thr Pro Ala Val Ser Val Ala		
	420	425	430
25	Ala Ser Leu Pro Asp Val Pro Pro Leu Leu Leu Ser Ala Arg Ser Glu		
	435	440	445
	Gly Ala Leu Arg Ala Gln Ala Val Arg Leu Gly Glu Tyr Val Glu Arg		
	450	455	460
30	Val Gly Ala Asp Pro Arg Asp Val Ala Tyr Ser Leu Ala Ser Thr Arg		
	465	470	475
	480		
	Thr Leu Phe Glu His Arg Ala Val Val Pro Cys Gly Gly Arg Gly Glu		
35	485	490	495
	Leu Val Ala Ala Leu Gly Gly Phe Ala Ala Gly Arg Val Ser Gly Gly		
	500	505	510
	515		
	520		
	525		
40	Val Arg Ser Gly Arg Ala Val Pro Gly Gly Val Gly Val Leu Phe Thr		
	530	535	540
	545		
	550		
	555		
	560		
45	Gly Gly Val Phe Ala Glu Val Leu Asp Glu Val Leu Ser Met Val Gly		
	565	570	575
	580		
	585		
	590		
50	Val Asp Ala Gly Ala Gly Ala Asp Ala Gly Ala Gly Ala Gly		
	595	600	605
	610		
	615		
	620		

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Leu Glu Ala Arg Gly Val Glu Val Ser Val Val Leu Gly His Ser Val
 625 630 635 640

5 Gly Glu Val Ala Ala Ala Tyr Val Ala Gly Val Leu Ser Leu Gly Asp
 645 650 655

Ala Val Arg Leu Val Val Ala Arg Gly Gly Leu Met Gly Gly Leu Pro
 660 665 670

10 Val Gly Gly Gly Met Trp Ser Val Gly Ala Ser Glu Ser Val Val Arg
 675 680 685

Gly Val Val Glu Gly Leu Gly Glu Trp Val Ser Val Ala Ala Val Asn
 690 695 700

15 Gly Pro Arg Ser Val Val Leu Ser Gly Asp Val Gly Val Leu Glu Ser
 705 710 715 720

Val Val Ala Ser Leu Met Gly Asp Gly Val Glu Cys Arg Arg Leu Asp
 20 725 730 735

Val Ser His Gly Phe His Ser Val Leu Met Glu Pro Val Leu Gly Glu
 740 745 750

25 Phe Arg Gly Val Val Glu Ser Leu Glu Phe Gly Arg Val Arg Pro Gly
 755 760 765

Val Val Val Val Ser Gly Val Ser Gly Gly Val Val Gly Ser Gly Glu
 770 775 780

30 Leu Gly Asp Pro Gly Tyr Trp Val Arg His Ala Arg Glu Ala Val Arg
 785 790 795 800

Phe Ala Asp Gly Val Gly Val Val Arg Gly Leu Gly Val Gly Thr Leu
 805 810 815

35 Val Glu Val Gly Pro His Gly Val Leu Thr Gly Met Ala Gly Glu Cys
 820 825 830

Leu Gly Ala Gly Asp Asp Val Val Val Val Pro Ala Met Arg Arg Gly
 835 840 845

40 Arg Ala Glu Arg Glu Val Phe Glu Ala Ala Leu Ala Thr Val Phe Thr
 850 855 860

Arg Asp Ala Gly Leu Asp Ala Thr Ala Leu His Thr Gly Ser Thr Gly
 865 870 875 880

45 Arg Arg Ile Asp Leu Pro Thr Tyr Pro Phe Gln Arg Arg Thr His Trp
 885 890 895

Ser Pro Ala Leu Ser Arg Pro Val Thr Ala Asp Ala Gly Ala Gly Val
 900 905 910

50 Thr Ala Thr Asp Ala Val Gly His Ser Val Ser Pro Asp Pro Glu Ser
 915 920 925

Thr Glu Gly Thr Ser His Arg Asp Thr Asp Asp Glu Ala Asp Ser Ala
 55 930 935 940

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Ser Pro Glu Pro Met Ser Pro Glu Asp Ala Val Arg Leu Val Arg Glu
 945 950 955 960
 5 Ser Thr Ala Ala Val Leu Gly His Asp Asp Pro Gly Glu Val Ala Leu
 965 970 975
 Asp Arg Thr Phe Thr Ser Gln Gly Met Asp Ser Val Thr Ala Val Glu
 980 985 990
 10 Leu Cys Asp Leu Leu Lys Gly Ala Ser Gly Leu Pro Leu Ala Ala Thr
 995 1000 1005
 Leu Val Tyr Asp Leu Pro Thr Pro Arg Ala Val Ala Glu His Ile Val
 1010 1015 1020
 15 Glu Ala Ala Gly Gly Pro Lys Asp Ser Val Ala Gly Gly Pro Gly Val
 1025 1030 1035 1040
 Leu Ser Ser Ala Ala Val Gly Val Ser Asp Ala Arg Gly Gly Ser Arg
 1045 1050 1055
 20 Asp Asp Asp Asp Pro Ile Ala Ile Val Gly Val Gly Cys Arg Leu Pro
 1060 1065 1070
 Gly Gly Val Asp Ser Arg Ala Ala Leu Trp Glu Leu Leu Glu Ser Gly
 25 1075 1080 1085
 Ala Asp Ala Ile Ser Ser Phe Pro Thr Asp Arg Gly Trp Asp Leu Asp
 1090 1095 1100
 Gly Leu Tyr Asp Pro Glu Pro Gly Thr Pro Gly Lys Thr Tyr Val Arg
 30 1105 1110 1115 1120
 Glu Gly Gly Phe Leu His Ser Ala Ala Glu Phe Asp Ala Glu Phe Phe
 1125 1130 1135
 35 Gly Ile Ser Pro Arg Glu Ala Thr Ala Met Asp Pro Gln Gln Arg Leu
 1140 1145 1150
 Leu Leu Glu Ala Ser Trp Glu Ala Leu Glu Asp Ala Gly Val Leu Pro
 40 1155 1160 1165
 Glu Ser Leu Arg Gly Gly Asp Ala Gly Val Phe Val Gly Ala Thr Ala
 1170 1175 1180
 Pro Glu Tyr Gly Pro Arg Leu His Glu Gly Ala Asp Gly Tyr Glu Gly
 45 1185 1190 1195 1200
 Tyr Leu Leu Thr Gly Thr Thr Ala Ser Val Ala Ser Gly Arg Ile Ala
 1205 1210 1215
 Tyr Thr Leu Gly Thr Gly Gly Pro Ala Leu Thr Val Asp Thr Ala Cys
 50 1220 1225 1230
 Ser Ser Ser Leu Val Ala Leu His Leu Ala Val Gln Ala Leu Arg Arg
 1235 1240 1245
 Gly Glu Cys Gly Leu Ala Leu Ala Gly Gly Ala Thr Val Met Ser Gly
 55 1250 1255 1260
 Pro Gly Met Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp

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	1265	1270	1275	1280
	Gly Arg Cys Met Pro Phe Ser Ala Asp Ala Asp Gly Thr Ala Trp Ser			
5	1285		1290	1295
	Glu Gly Val Ala Val Leu Ala Leu Glu Arg Leu Ser Asp Ala Arg Arg			
	1300		1305	1310
10	Ala Gly His Arg Val Leu Gly Val Val Arg Gly Ser Ala Val Asn Gln			
	1315		1320	1325
	Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Arg Ser Ala Gln Glu			
	1330		1335	1340
15	Gly Val Ile Arg Ala Ala Leu Ala Asp Ala Gly Leu Ala Pro Gly Asp			
	1345		1350	1355
	Val Asp Ala Val Glu Ala His Gly Thr Gly Thr Ala Leu Gly Asp Pro			
	1365		1370	1375
20	Ile Glu Ala Ser Ala Leu Leu Ala Thr Tyr Gly Arg Glu Arg Val Gly			
	1380		1385	1390
	Asp Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Val Gly His Thr Gln			
	1395		1400	1405
25	Ala Ala Ala Gly Ala Ala Gly Val Val Lys Met Leu Leu Ala Leu Glu			
	1410		1415	1420
	His Gly Thr Leu Pro Arg Thr Leu His Ala Asp Arg Pro Ser Thr His			
	1425		1430	1435
30	1440		1445	1440
	Val Asp Trp Ser Ser Gly Thr Val Ala Leu Leu Ala Glu Ala Arg Arg			
	1445		1450	1455
	Trp Pro Arg Arg Ser Asp Arg Pro Arg Arg Ala Ala Val Ser Ser Phe			
35	1460		1465	1470
	Gly Ile Ser Gly Thr Asn Ala His Leu Ile Ile Glu Glu Ala Pro Glu			
	1475		1480	1485
40	Trp Val Glu Asp Ile Asp Gly Val Ala Ala Pro Asp Arg Gly Thr Ala			
	1490		1495	1500
	Asp Ala Ala Ala Pro Ser Pro Leu Leu Leu Ser Ala Arg Ser Glu Gly			
	1505		1510	1515
45	1520		1525	1530
	Ala Leu Arg Ala Gln Ala Val Arg Leu Gly Glu Tyr Val Glu Arg Val			
	1535		1530	1535
	Gly Ala Asp Pro Arg Asp Val Ala Tyr Ser Leu Ala Ser Thr Arg Thr			
	1540		1545	1550
50	Leu Phe Glu His Arg Ala Val Val Pro Cys Gly Gly Arg Gly Glu Leu			
	1555		1560	1565
	Val Ala Ala Leu Gly Gly Phe Ala Ala Gly Arg Val Ser Gly Gly Val			
	1570		1575	1580
55	Arg Ser Gly Arg Ala Val Pro Gly Gly Val Gly Val Leu Phe Thr Gly			
	1585		1590	1595
	1600			

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Gln Gly Ala Gln Trp Val Gly Met Gly Arg Gly Leu Tyr Ala Gly Gly
 1605 1610 1615
 5 Gly Val Phe Ala Glu Val Leu Asp Glu Val Leu Ser Met Val Gly Glu
 1620 1625 1630
 Val Asp Gly Arg Ser Leu Arg Asp Val Met Phe Gly Asp Val Asp Val
 1635 1640 1645
 10 Asp Ala Gly Ala Gly Ala Asp Ala Gly Ala Gly Ala Gly Val
 1650 1655 1660
 Gly Ser Gly Ser Gly Ser Val Gly Gly Leu Leu Gly Arg Thr Glu Phe
 1665 1670 1675 1680
 15 Ala Gln Pro Ala Leu Phe Ala Leu Glu Val Ala Leu Phe Arg Ala Leu
 1685 1690 1695
 Glu Ala Arg Gly Val Glu Val Ser Val Val Leu Gly His Ser Val Gly
 20 1700 1705 1710
 Glu Val Ala Ala Ala Tyr Val Ala Gly Val Leu Ser Leu Gly Asp Ala
 1715 1720 1725
 25 Val Arg Leu Val Val Ala Arg Gly Gly Leu Met Gly Gly Leu Pro Val
 1730 1735 1740
 Gly Gly Gly Met Trp Ser Val Gly Ala Ser Glu Ser Val Val Arg Gly
 1745 1750 1755 1760
 30 Val Val Glu Gly Leu Gly Glu Trp Val Ser Val Ala Ala Val Asn Gly
 1765 1770 1775
 Pro Arg Ser Val Val Leu Ser Gly Asp Val Gly Val Leu Glu Ser Val
 1780 1785 1790
 35 Val Ala Ser Leu Met Gly Asp Gly Val Glu Cys Arg Arg Leu Asp Val
 1795 1800 1805
 Ser His Gly Phe His Ser Val Leu Met Glu Pro Val Leu Gly Glu Phe
 1810 1815 1820
 40 Arg Gly Val Val Glu Ser Leu Glu Phe Gly Arg Val Arg Pro Gly Val
 1825 1830 1835 1840
 Val Val Val Ser Gly Val Ser Gly Gly Val Val Gly Ser Gly Glu Leu
 45 1845 1850 1855
 Gly Asp Pro Gly Tyr Trp Val Arg His Ala Arg Glu Ala Val Arg Phe
 1860 1865 1870
 Ala Asp Gly Val Gly Val Val Arg Gly Leu Gly Val Gly Thr Leu Val
 50 1875 1880 1885
 Glu Val Gly Pro His Gly Val Leu Thr Gly Met Ala Gly Glu Cys Leu
 1890 1895 1900
 Gly Ala Gly Asp Asp Val Val Val Val Pro Ala Met Arg Arg Gly Arg
 55 1905 1910 1915 1920

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Ala Glu Arg Glu Val Phe Glu Ala Ala Leu Ala Thr Val Phe Thr Arg
 1925 1930 1935
 Asp Ala Gly Leu Asp Ala Thr Ala Leu His Thr Gly Ser Thr Gly Arg
 1940 1945 1950
 Arg Ile Asp Leu Pro Thr Tyr Pro Phe Gln Arg Asp Arg Tyr Trp Leu
 1955 1960 1965
 10 Asp Pro Val Arg Thr Ala Val Thr Gly Val Glu Pro Ala Gly Ser Pro
 1970 1975 1980
 Ala Asp Ala Arg Ala Thr Glu Arg Gly Arg Ser Thr Thr Ala Gly Ile
 1985 1990 1995 2000
 15 Arg Tyr Arg Val Ala Trp Gln Pro Ala Val Val Asp Arg Gly Asn Pro
 2005 2010 2015
 Gly Pro Ala Gly His Val Leu Leu Leu Ala Pro Asp Glu Asp Thr Ala
 2020 2025 2030
 20 Asp Ser Gly Leu Ala Pro Ala Ile Ala Arg Glu Leu Ala Val Arg Gly
 2035 2040 2045
 Ala Glu Val His Thr Val Ala Val Pro Val Gly Thr Gly Arg Glu Ala
 2050 2055 2060
 25 Ala Gly Asp Leu Leu Arg Ala Ala Gly Asp Gly Ala Ala Arg Ser Thr
 2065 2070 2075 2080
 Arg Val Leu Trp Leu Ala Pro Ala Glu Pro Asp Ala Ala Asp Ala Val
 30 2085 2090 2095
 Ala Leu Val Gln Ala Leu Gly Glu Ala Val Pro Glu Ala Pro Leu Trp
 2100 2105 2110
 35 Ile Thr Thr Arg Glu Ala Ala Ala Val Arg Pro Asp Glu Thr Pro Ser
 2115 2120 2125
 Val Gly Gly Ala Gln Leu Trp Gly Leu Gly Gln Val Ala Ala Leu Glu
 2130 2135 2140
 40 Leu Gly Arg Arg Trp Gly Gly Leu Ala Asp Leu Pro Gly Ser Ala Ser
 2145 2150 2155 2160
 Pro Ala Val Leu Arg Thr Phe Val Gly Ala Leu Leu Ala Gly Gly Glu
 2165 2170 2175
 45 Asn Gln Phe Ala Val Arg Pro Ser Gly Val His Val Arg Arg Val Val
 2180 2185 2190
 Pro Ala Pro Val Pro Val Pro Ala Ser Ala Arg Thr Val Thr Thr Ala
 2195 2200 2205
 50 Pro Ala Thr Ala Val Gly Glu Asp Ala Arg Asn Asn Asp Thr Ser Asp Val
 2210 2215 2220
 Val Val Pro Asp Asp Arg Trp Ser Ser Gly Thr Val Leu Ile Thr Gly
 55 2225 2230 2235 2240

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Gly Thr Gly Ala Leu Gly Ala Gln Val Ala Arg Arg Leu Ala Arg Ser
 2245 2250 2255
 Gly Ala Ala Arg Leu Leu Leu Val Gly Arg Arg Gly Ala Ala Gly Pro
 2260 2265 2270
 5
 Gly Val Gly Glu Leu Val Glu Glu Leu Thr Ala Leu Gly Ser Glu Val
 2275 2280 2285
 Ala Val Glu Ala Cys Asp Val Ala Asp Arg Asp Ala Leu Ala Leu
 10 2290 2295 2300
 Leu Ala Gly Leu Pro Glu Glu Arg Pro Leu Val Ala Val Leu His Ala
 2305 2310 2315 2320
 Ala Gly Val Leu Asp Asp Gly Val Leu Asp Ser Leu Thr Ser Asp Arg
 15 2325 2330 2335
 Val Asp Ala Val Leu Arg Asp Lys Val Thr Ala Ala Arg His Leu Asp
 2340 2345 2350
 20 Glu Leu Thr Ala Asp Leu Pro Leu Asp Ala Phe Val Leu Phe Ser Ser
 2355 2360 2365
 Ile Val Gly Val Trp Gly Asn Gly Gly Gln Ala Val Tyr Ala Ala Ala
 2370 2375 2380
 25 Asn Ala Ala Leu Asp Ala Leu Ala Gln Arg Arg Arg Ala Arg Gly Ala
 2385 2390 2395 2400
 Arg Ala Ala Ser Ile Ala Trp Gly Pro Trp Ala Gly Ala Gly Met Ala
 2405 2410 2415
 30 Ser Gly Thr Ala Ala Lys Ser Phe Glu Arg Asp Gly Val Thr Ala Leu
 2420 2425 2430
 Asp Pro Glu Arg Ala Leu Asp Val Leu Asp Asp Val Val Gly Ala Gly
 35 2435 2440 2445
 Gly Thr Ser Ala Ala Gly Thr His Ala Ala Gly Glu Ser Ser Leu Leu
 2450 2455 2460
 Val Ala Asp Val Asp Trp Glu Thr Phe Val Gly Arg Ser Val Thr Arg
 40 2465 2470 2475 2480
 Arg Thr Trp Ser Leu Phe Asp Gly Val Ser Ala Ala Arg Ser Ala Arg
 2485 2490 2495
 Ala Gly His Ala Ala Asp Asp Arg Ala Ala Leu Thr Pro Gly Thr Arg
 45 2500 2505 2510
 Pro Gly Asp Gly Ala Pro Gly Gly Ser Gly Gln Asp Gly Glu Gly
 2515 2520 2525
 Arg Pro Trp Leu Ser Val Gly Pro Ser Pro Ala Glu Arg Arg Arg Ala
 50 2530 2535 2540
 Leu Leu Thr Leu Val Arg Ser Glu Ala Ala Gly Ile Leu Arg His Ala
 2545 2550 2555 2560
 55 Ser Ala Asp Ala Val Asp Pro Glu Leu Ala Phe Arg Ser Ala Gly Phe

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	2565	2570	2575
	Asp Ser Leu Thr Val Leu Glu Leu Arg Asn Arg Leu Thr Ala Ala Thr 2580	2585	2590
5	Gly Leu Asn Leu Pro Asn Thr Leu Leu Phe Asp His Pro Thr Pro Leu 2595	2600	2605
	Ser Leu Ala Ser His Leu His Asp Glu Leu Phe Gly Pro Asp Ser Glu 2610	2615	2620
10	Ala Glu Pro Ala Ala Ala Pro Thr Pro Val Met Ala Asp Glu Arg 2625	2630	2635
	Glu Pro Ile Ala Ile Val Gly Met Ala Cys Arg Tyr Pro Gly Gly Val 2645	2650	2655
15	Ala Ser Pro Asp Asp Leu Trp Asp Leu Val Ala Gly Asp Gly His Thr 2660	2665	2670
	Leu Ser Pro Phe Pro Ala Asp Arg Gly Trp Asp Val Glu Gly Leu Tyr 2675	2680	2685
20	Asp Pro Glu Pro Gly Val Pro Gly Lys Ser Tyr Val Arg Glu Gly Gly 2690	2695	2700
	Phe Leu Arg Ser Ala Ala Glu Phe Asp Ala Glu Phe Phe Gly Ile Ser 2705	2710	2715
25	Pro Arg Glu Ala Thr Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu 2725	2730	2735
	Thr Ser Trp Glu Ala Leu Glu Arg Ala Gly Ile Val Pro Asp Ser Leu 2740	2745	2750
30	Arg Gly Thr Arg Thr Gly Val Phe Ser Gly Ile Ser Gln Gln Asp Tyr 2755	2760	2765
	Ala Thr Gln Leu Gly Asp Ala Ala Asp Thr Tyr Gly Gly His Val Leu 2770	2775	2780
35	Thr Gly Thr Leu Gly Ser Val Ile Ser Gly Arg Val Ala Tyr Ala Leu 2785	2790	2800
	Gly Leu Glu Gly Pro Ala Leu Thr Val Asp Thr Ala Cys Ser Ser Ser 2805	2810	2815
40	Leu Val Ala Leu His Leu Ala Val Gln Ser Leu Arg Arg Gly Glu Cys 2820	2825	2830
	Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met Ala Thr Pro Thr Val 2835	2840	2845
45	Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Ala Asp Gly Arg Cys 2850	2855	2860
	Lys Ala Phe Ala Glu Gly Ala Asp Gly Thr Ala Trp Ala Glu Gly Val 2865	2870	2880
50	Gly Val Leu Leu Val Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly His 2885	2890	2895

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Arg Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly Ala
 2900 2905 2910
 5 Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ala Gln Gln Arg Val Ile
 2915 2920 2925
 Arg Glu Ala Leu Ala Asp Ala Gly Leu Val Pro Ala Asp Val Asp Val
 2930 2935 2940
 10 Val Glu Ala His Gly Thr Gly Thr Ala Leu Gly Asp Pro Ile Glu Ala
 2945 2950 2955 2960
 Gly Ala Leu Leu Ala Thr Tyr Gly Arg Glu Arg Val Gly Asp Pro Leu
 2965 2970 2975
 15 Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln Ala Ala Ala
 2980 2985 2990
 Gly Val Gly Gly Val Ile Lys Val Val Gln Gly Met Arg His Gly Ser
 2995 3000 3005
 20 Leu Pro Arg Thr Leu His Val Asp Ala Pro Ser Ser Lys Val Glu Trp
 3010 3015 3020
 Ala Ser Gly Ala Val Glu Leu Leu Thr Glu Thr Arg Ser Trp Pro Arg
 3025 3030 3035 3040
 25 Arg Val Glu Arg Val Arg Arg Ala Ala Val Ser Ala Phe Gly Val Ser
 3045 3050 3055
 Gly Thr Asn Ala His Val Val Leu Glu Glu Ala Pro Ala Glu Ala Gly
 3060 3065 3070
 30 Ser Glu His Gly Asp Gly Pro Glu Pro Glu Arg Pro Asp Ala Val Thr
 3075 3080 3085
 Gly Pro Leu Ser Trp Val Leu Ser Ala Arg Ser Glu Gly Ala Leu Arg
 3090 3095 3100
 35 Ala Gln Ala Val Arg Leu Arg Glu Cys Val Glu Arg Val Gly Ala Asp
 3105 3110 3115 3120
 40 Pro Arg Asp Val Ala Gly Ser Leu Val Val Ser Arg Ala Ser Phe Gly
 3125 3130 3135
 Glu Arg Ala Val Val Val Gly Arg Gly Arg Glu Glu Leu Leu Ala Gly
 3140 3145 3150
 45 Leu Asp Val Val Ala Ala Gly Ala Pro Val Gly Val Ser Ser Gly Ala
 3155 3160 3165
 Gly Ala Val Val Arg Gly Ser Ala Val Arg Gly Arg Gly Val Gly Val
 3170 3175 3180
 50 Leu Phe Thr Gly Gln Gly Ala Gln Trp Val Gly Met Gly Arg Gly Leu
 3185 3190 3195 3200
 Tyr Ala Gly Gly Val Phe Ala Glu Val Leu Asp Glu Val Leu Ser
 3205 3210 3215
 55

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Val Val Gly Glu Val Asp Gly Arg Ser Leu Arg Asp Val Met Phe Ala
 3220 3225 3230
 Asp Ala Asp Ser Val Leu Gly Gly Leu Leu Gly Arg Thr Glu Phe Ala
 5 3235 3240 3245
 Gln Pro Ala Leu Phe Ala Leu Glu Val Ala Leu Phe Arg Ala Leu Glu
 3250 3255 3260
 Ala Arg Gly Val Glu Val Ser Val Val Leu Gly His Ser Val Gly Glu
 10 3265 3270 3275 3280
 Val Ala Ala Ala Tyr Val Ala Gly Val Leu Ser Leu Gly Asp Ala Val
 3285 3290 3295
 Arg Leu Val Val Ala Arg Gly Gly Leu Met Gly Gly Leu Pro Val Gly
 15 3300 3305 3310
 Gly Gly Met Trp Ser Val Gly Ala Ser Glu Ser Val Val Arg Gly Val
 3315 3320 3325
 Val Glu Gly Leu Gly Glu Trp Val Ser Val Ala Ala Val Asn Gly Pro
 20 3330 3335 3340
 Arg Ser Val Val Leu Ser Gly Asp Val Gly Val Leu Glu Ser Val Val
 3345 3350 3355 3360
 Val Thr Leu Met Gly Asp Gly Val Glu Cys Arg Arg Leu Asp Val Ser
 25 3365 3370 3375
 His Gly Phe His Ser Val Leu Met Glu Pro Val Leu Gly Glu Phe Arg
 3380 3385 3390
 Gly Val Val Glu Ser Leu Glu Phe Gly Arg Val Arg Pro Gly Val Val
 30 3395 3400 3405
 Val Val Ser Gly Val Ser Gly Gly Val Val Gly Ser Gly Glu Leu Gly
 3410 3415 3420
 Asp Pro Gly Tyr Trp Val Arg His Ala Arg Glu Ala Val Arg Phe Ala
 35 3425 3430 3435 3440
 Asp Gly Val Gly Val Val Arg Gly Leu Gly Val Gly Thr Leu Val Glu
 40 3445 3450 3455
 Val Gly Pro His Gly Val Leu Thr Gly Met Ala Gly Gln Cys Leu Glu
 3460 3465 3470
 Ala Gly Asp Asp Val Val Val Pro Ala Met Arg Arg Gly Arg Pro
 45 3475 3480 3485
 Glu Arg Glu Val Phe Glu Ala Ala Leu Ala Thr Val Phe Thr Arg Asp
 3490 3495 3500
 Ala Gly Leu Asp Ala Thr Thr Leu His Thr Gly Ser Thr Gly Arg Arg
 50 3505 3510 3515 3520
 Ile Asp Leu Pro Thr Tyr Pro Phe Gln His Asn Arg Tyr Trp Ala Thr
 3525 3530 3535
 Gly Ser Val Thr Gly Ala Thr Gly Thr Ser Ala Ala Arg Phe Gly

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	3540	3545	3550
	Leu Glu Trp Lys Asp His Pro Phe Leu Ser Gly Ala Thr Pro Ile Ala		
5	3555	3560	3565
	Gly Ser Gly Ala Leu Leu Leu Thr Gly Arg Val Gly Leu Ala Ala His		
	3570	3575	3580
10	Pro Trp Leu Ala Asp His Ala Ile Ser Gly Thr Val Leu Leu Pro Gly		
	3585	3590	3595
	Thr Ala Ile Ala Asp Leu Leu Leu Arg Ala Val Glu Glu Val Gly Ala		
	3605	3610	3615
15	Gly Gly Val Glu Glu Leu Thr Leu His Glu Pro Leu Leu Pro Glu		
	3620	3625	3630
20	Arg Gly Gly Leu His Val Gln Val Leu Val Glu Ala Ala Asp Glu Gln		
	3635	3640	3645
	Gly Arg Arg Ala Val Ala Val Ala Ala Arg Pro Glu Gly Pro Gly Arg		
	3650	3655	3660
	Asp Gly Glu Glu Gln Glu Trp Thr Arg His Ala Glu Gly Val Leu Thr		
	3665	3670	3675
	3680		
25	Ser Thr Glu Thr Ala Val Pro Asp Met Gly Trp Ala Ala Gly Ala Trp		
	3685	3690	3695
	Pro Pro Pro Gly Ala Glu Pro Ile Asp Val Glu Glu Leu Tyr Asp Ala		
	3700	3705	3710
30	Phe Ala Ala Asp Gly Tyr Gly Tyr Gly Pro Ala Phe Thr Ala Leu Ser		
	3715	3720	3725
	Gly Val Trp Arg Leu Gly Asp Glu Leu Phe Ala Glu Val Arg Arg Pro		
	3730	3735	3740
35	Ala Gly Gly Ala Gly Thr Thr Gly Asp Gly Phe Gly Val His Pro Ala		
	3745	3750	3755
	3760		
	Leu Phe Asp Ala Ala Leu His Pro Trp Arg Ala Gly Gly Leu Leu Pro		
	3765	3770	3775
40	Asp Thr Gly Gly Thr Thr Trp Ala Pro Phe Ser Trp Gln Gly Ile Ala		
	3780	3785	3790
	Leu His Thr Thr Gly Ala Glu Thr Leu Arg Val Arg Leu Ala Pro Ala		
45	3795	3800	3805
	Ala Gly Gly Thr Glu Ser Ala Phe Ser Val Gln Ala Ala Asp Pro Ala		
	3810	3815	3820
50	Gly Thr Pro Val Leu Thr Leu Asp Ala Leu Leu Leu Arg Pro Val Thr		
	3825	3830	3840
	Leu Gly Arg Ala Asp Ala Pro Gln Pro Leu Tyr Arg Val Asp Trp Gln		
	3845	3850	3855
55	Pro Val Gly Gln Gly Thr Glu Ala Ser Gly Ala Gln Gly Trp Thr Val		
	3860	3865	3870

Leu Gly Gln Ala Ala Ala Glu Thr Val Ala Gln Pro Ala Ala His Ala,
 3875 3880 3885
 5 Asp Leu Thr Ala Leu Arg Thr Ala Val Ala Ala Gly Thr Pro Val
 3890 3895 3900
 Pro Arg Leu Val Val Val Ser Pro Val Asp Thr Arg Leu Asp Glu Gly
 3905 3910 3915 3920
 10 Pro Val Leu Ala Asp Ala Glu Ala Arg Ala Arg Ala Gly Asp Gly Trp
 3925 3930 3935
 Asp Asp Asp Pro Leu Arg Val Ala Leu Gly Arg Gly Leu Thr Leu Val
 3940 3945 3950
 15 Arg Glu Trp Val Glu Asp Glu Arg Leu Ala Asp Ser Arg Leu Val Val
 3955 3960 3965
 Leu Thr Arg Gly Ala Val Ala Ala Gly Pro Gly Asp Val Pro Asp Leu
 20 3970 3975 3980
 Thr Gly Ala Ala Leu Trp Gly Leu Leu Arg Ser Ala Gln Ser Glu Tyr
 3985 3990 3995 4000
 25 Pro Asp Arg Phe Thr Leu Ile Asp Val Asp Asp Ser Pro Glu Ser Arg
 4005 4010 4015
 Ala Ala Leu Pro Arg Ala Leu Gly Ser Ala Glu Arg Gln Leu Ala Leu
 4020 4025 4030
 Arg Thr Gly Asp Val Leu Ala Pro Ala Leu Val Pro Met Ala Thr Arg
 30 4035 4040 4045
 Pro Ala Glu Thr Thr Pro Ala Thr Ala Val Ala Ser Ala Thr Thr Gln
 4050 4055 4060
 35 Thr Gln Val Thr Ala Pro Ala Pro Asp Asp Pro Ala Ala Asp Ala Val
 4065 4070 4075 4080
 Phe Asp Pro Ala Gly Thr Val Leu Ile Thr Gly Gly Thr Gly Ala Leu
 4085 4090 4095
 40 Gly Arg Arg Val Ala Ser His Leu Ala Arg Arg Tyr Gly Val Arg His
 4100 4105 4110
 Met Leu Leu Val Ser Arg Arg Gly Pro Asp Ala Pro Glu Ala Gly Pro
 4115 4120 4125
 45 Leu Glu Arg Glu Leu Ala Gly Leu Gly Val Thr Ala Thr Phe Leu Ala
 4130 4135 4140
 Cys Asp Leu Thr Asp Ile Glu Ala Val Arg Lys Ala Val Ala Ala Val
 4145 4150 4155 4160
 50 Pro Ser Asp His Pro Leu Thr Gly Val Val His Thr Ala Gly Val Leu
 4165 4170 4175
 Asp Asp Gly Ala Leu Thr Gly Leu Thr Arg Gln Arg Leu Asp Thr Val
 55 4180 4185 4190

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Leu Arg Pro Lys Ala Asp Ala Val Arg Asn Leu His Glu Ala Thr Leu
 4195 4200 4205
 5 Asp Arg Pro Leu Arg Ala Phe Val Leu Phe Ser Ala Ala Ala Gly Leu
 4210 4215 4220
 Leu Gly Arg Pro Gly Gln Ala Ser Tyr Ala Ala Ala Asn Ala Val Leu
 4225 4230 4235 4240
 10 Asp Ala Leu Ala Gly Ala Arg Arg Ala Ala Gly Leu Pro Ala Val Ser
 4245 4250 4255
 Leu Ala Trp Gly Leu Trp Asp Glu Gln Thr Gly Met Ala Gly Gly Leu
 4260 4265 4270
 15 Asp Glu Met Ala Leu Arg Val Leu Arg Arg Asp Gly Ile Ala Ala Met
 4275 4280 4285
 Pro Pro Glu Gln Gly Leu Glu Leu Leu Asp Leu Ala Leu Thr Gly His
 4290 4295 4300
 20 Arg Asp Gly Pro Ala Val Leu Val Pro Leu Leu Leu Asp Gly Ala Ala
 4305 4310 4315 4320
 Leu Arg Arg Thr Ala Lys Glu Arg Gly Ala Ala Thr Met Ser Pro Leu
 4325 4330 4335
 25 Leu Arg Ala Leu Leu Pro Ala Ala Leu Arg Arg Ser Gly Gly Ala Gly
 4340 4345 4350
 Ala Pro Ala Ala Ala Asp Arg His Gly Lys Glu Ala Asp Pro Gly Ala
 30 4355 4360 4365
 Gly Arg Leu Ala Gly Met Val Ala Leu Glu Ala Ala Glu Arg Ser Ala
 4370 4375 4380
 Ala Val Leu Glu Leu Val Thr Glu Gln Val Ala Glu Val Leu Gly Tyr
 35 4385 4390 4395 4400
 Ala Ser Ala Ala Glu Ile Glu Pro Glu Arg Pro Phe Arg Glu Ile Gly
 4405 4410 4415
 Val Asp Ser Leu Ala Ala Val Glu Leu Arg Asn Arg Leu Ser Arg Leu
 40 4420 4425 4430
 Val Gly Leu Arg Leu Pro Thr Thr Leu Ser Phe Asp His Pro Thr Pro
 4435 4440 4445
 45 Lys Asp Met Ala Gln His Ile Asp Gly Gln Leu Pro Arg Pro Ala Gly
 4450 4455 4460
 Ala Ser Pro Ala Asp Ala Ala Leu Glu Gly Ile Gly Asp Leu Ala Arg
 4465 4470 4475 4480
 50 Ala Val Ala Leu Leu Gly Thr Gly Asp Ala Arg Arg Ala Glu Val Arg
 4485 4490 4495
 Glu Gln Leu Val Gly Leu Leu Ala Ala Leu Asp Pro Pro Gly Arg Thr
 4500 4505 4510
 55 Gly Thr Ala Ala Pro Gly Val Pro Ser Gly Ala Asp Gly Ala Glu Pro

4515 4520 4525

5 Thr Val Thr Asp Arg Leu Asp Glu Ala Thr Asp Asp Glu Ile Phe Ala
 4530 4535 4540

Phe Leu Asp Glu Gln Leu
 4545 4550

(2) INFORMATION FOR SEQ ID NO:9:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1996 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

- 16 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

20 Met Thr Ala Glu Asn Asp Lys Ile Arg Ser Tyr Leu Lys Arg Ala Thr
 1 5 10 15

Ala Glu Leu His Arg Thr Lys Ser Arg Leu Ala Glu Val Glu Ser Ala
 20 25 30

25 Ser Arg Glu Pro Ile Ala Ile Val Gly Met Ala Cys Arg Tyr Pro Gly
 35 40

Gly Val Ala Ser Pro Asp Asp Leu Trp Asp Leu Val Ala Ala Gly Thr
 50 55 60

Asp Ala Val Ser Ala Phe Pro Val Asp Arg Gly Trp Asp Val Glu Gly
 65 70 75 80

Leu Tyr Asp Pro Asp Pro Glu Ala Val Gly Arg Ser Tyr Val Arg Glu
 85 90 95

35 Gly Gly Phe Leu His Ser Ala Ala Glu Phe Asp Ala Glu Phe Phe Gly
 100 105 110

40 Ile Ser Pro Arg Glu Ala Ala Met Asp Pro Gln Gln Arg Leu Leu
 115 120 125

Leu Glu Thr Ser Trp Glu Ala Leu Glu Arg Ala Gly Ile Val Pro Ala
 130 135 140

45 Ser Leu Arg Gly Thr Arg Thr Gly Val Phe Thr Gly Val Met Tyr Asp
 145 150 155 160

Asp Tyr Gly Ser Arg Phe Asp Ser Ala Pro Pro Glu Tyr Glu Gly Tyr
 165 170 175

50 Leu Val Asn Gly Ser Ala Gly Ser Ile Ala Ser Gly Arg Val Ala Tyr
 180 185 190

Ala Leu Gly Leu Glu Gly Pro Ala Leu Thr Val Asp Thr Ala Cys Ser
 195 200 205

55 Ser Ser Leu Val Ala Leu His Leu Ala Val Gln Ser Leu Arg Arg Gly

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	210	215	220
	Glu Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met Ala Thr Pro		
5	225	230	235
	240		
	Thr Val Leu Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Ala Asp Gly		
	245	250	255
	Arg Cys Lys Ala Phe Ala Glu Gly Ala Asp Gly Thr Ala Trp Ala Glu		
10	260	265	270
	Gly Val Gly Val Leu Leu Val Glu Arg Leu Ser Asp Ala Arg Arg Asn		
	275	280	285
15	Gly His Arg Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln Asp		
	290	295	300
	Gly Ala Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ala Gln Gln Arg		
	305	310	315
	320		
20	Val Ile Arg Glu Ala Leu Ala Asp Ala Gly Leu Thr Pro Ala Asp Val		
	325	330	335
	Asp Ala Val Glu Ala His Gly Thr Gly Thr Pro Leu Gly Asp Pro Ile		
	340	345	350
25	Glu Ala Gly Ala Leu Leu Ala Thr Tyr Gly Ser Glu Arg Gln Gln Gln		
	355	360	365
	Gly Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln		
	370	375	380
30	Ala Ala Ala Gly Val Gly Val Ile Lys Val Val Gln Ala Met Arg		
	385	390	395
	400		
35	His Gly Ser Leu Pro Arg Thr Leu His Val Asp Ala Pro Ser Ser Lys		
	405	410	415
	Val Glu Trp Ala Ser Gly Ala Val Glu Leu Leu Thr Glu Thr Arg Ser		
	420	425	430
	Trp Pro Arg Arg Val Glu Arg Val Arg Arg Ala Ala Val Ser Ala Phe		
	435	440	445
40	Gly Val Ser Gly Thr Asn Ala His Val Val Leu Glu Ala Pro Ala		
	450	455	460
	Glu Ala Gly Ser Glu His Gly Asp Gly Pro Glu Pro Glu Arg Pro Asp		
45	465	470	475
	480		
	Ala Val Thr Gly Pro Leu Ser Trp Val Leu Ser Ala Arg Ser Glu Gly		
	485	490	495
	Ala Leu Arg Ala Gln Ala Val Arg Leu Arg Glu Cys Val Glu Arg Val		
50	500	505	510
	Gly Ala Asp Pro Arg Asp Val Ala Gly Ser Leu Val Val Ser Arg Ala		
	515	520	525
55	Ser Phe Gly Glu Arg Ala Val Val Val Gly Arg Gly Arg Glu Glu Leu		
	530	535	540

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Leu Ala Gly Leu Asp Val Val Ala Ala Gly Ala Pro Val Gly Val Ser
545 550 555 560

5 Gly Gly Val Ser Ser Gly Ala Gly Ala Val Val Arg Gly Ser Ala Val
565 570 575

Arg Gly Arg Gly Val Gly Val Leu Phe Thr Gly Gln Gly Ala Gln Trp
580 585 590

10 Val Gly Met Gly Arg Gly Leu Tyr Ala Gly Gly Val Phe Ala Glu
595 600 605

Val Leu Asp Glu Val Leu Ser Val Val Gly Glu Val Gly Gly Trp Ser
610 615 620

15 Leu Arg Asp Val Met Phe Gly Asp Val Asp Val Asp Ala Gly Ala Gly
625 630 635 640

Ala Asp Ala Gly Val Gly Ser Gly Val Gly Val Gly Leu Leu Gly
20 645 650 655

Arg Thr Glu Phe Ala Gln Pro Ala Leu Phe Ala Leu Glu Val Ala Leu
660 665 670

25 Phe Arg Ala Leu Glu Ala Arg Gly Val Glu Val Ser Val Val Leu Gly
675 680 685

His Ser Val Gly Glu Val Ala Ala Ala Tyr Val Ala Gly Val Leu Ser
30 690 695 700

Leu Gly Asp Ala Val Arg Leu Val Val Ala Arg Gly Gly Leu Met Gly
705 710 715 720

Gly Leu Pro Val Gly Gly Met Trp Ser Val Gly Ala Ser Glu Ser
725 730 735

35 Val Val Arg Gly Val Val Glu Gly Leu Gly Glu Trp Val Ser Val Ala
740 745 750

Ala Val Asn Gly Pro Arg Ser Val Val Leu Ser Gly Asp Val Gly Val
40 755 760 765

Leu Glu Ser Val Val Ala Ser Leu Met Gly Asp Gly Val Glu Cys Arg
770 775 780

Arg Leu Asp Val Ser His Gly Phe His Ser Val Leu Met Glu Pro Val
785 790 795 800

45 Leu Gly Glu Phe Arg Gly Val Val Glu Ser Leu Glu Phe Gly Arg Val
805 810 815

Arg Pro Gly Val Val Val Val Ser Ser Val Ser Gly Gly Val Val Gly
50 820 825 830

Ser Gly Glu Leu Gly Asp Pro Gly Tyr Trp Val Arg His Ala Arg Glu
835 840 845

Ala Val Arg Phe Ala Asp Gly Val Gly Val Val Arg Gly Leu Gly Val
55 850 855 860

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Gly Thr Leu Val Glu Val Gly Pro His Gly Val Leu Thr Gly Met Ala
 865 870 875 880
 5 Gly Glu Cys Leu Gly Ala Gly Asp Asp Val Val Val Val Pro Ala Met
 885 890 895
 Arg Arg Gly Arg Ala Glu Arg Glu Val Phe Glu Ala Ala Leu Ala Thr
 900 905 910
 10 Val Phe Thr Arg Asp Ala Gly Leu Asp Ala Thr Thr Leu His Thr Gly
 915 920 925
 Ser Thr Gly Arg Arg Ile Asp Leu Pro Thr Tyr Pro Phe Gln His Asp
 930 935 940
 15 Arg Tyr Trp Leu Ala Ala Pro Ser Arg Pro Arg Thr Asp Gly Leu Ser
 945 950 955 960
 Ala Ala Gly Leu Arg Glu Val Glu His Pro Leu Leu Thr Ala Ala Val
 965 970 975
 20 Glu Leu Pro Gly Thr Asp Thr Glu Val Trp Thr Gly Arg Ile Ser Ala
 980 985 990
 Ala Asp Leu Pro Trp Leu Ala Asp His Leu Val Trp Asp Arg Gly Val
 995 1000 1005
 25 Val Pro Gly Thr Ala Leu Leu Glu Thr Val Leu Gln Val Gly Ser Arg
 1010 1015 1020
 Ile Gly Leu Pro Arg Val Ala Glu Leu Val Leu Glu Thr Pro Leu Thr
 1025 1030 1035 1040
 30 Trp Thr Ser Asp Arg Pro Leu Gln Val Arg Ile Val Val Thr Ala Ala
 1045 1050 1055
 Ala Thr Ala Pro Gly Gly Ala Arg Glu Leu Thr Leu His Ser Arg Pro
 35 1060 1065 1070
 Glu Pro Val Ala Ala Ser Ser Ser Pro Ser Pro Ala Ser Pro Arg
 1075 1080 1085
 40 His Leu Thr Ala Gln Glu Ser Asp Asp Asp Trp Thr Arg His Ala Ser
 1090 1095 1100
 Gly Leu Leu Ala Pro Ala Ala Gly Leu Ala Asp Asp Phe Ala Glu Leu
 1105 1110 1115 1120
 45 Thr Gly Ala Trp Pro Pro Val Gly Ala Glu Pro Leu Asp Leu Ala Gly
 1125 1130 1135
 Gln Tyr Pro Leu Phe Ala Ala Ala Gly Val Arg Tyr Glu Gly Ala Phe
 1140 1145 1150
 50 Arg Gly Leu Arg Ala Ala Trp Arg Arg Gly Asp Glu Val Phe Ala Asp
 1155 1160 1165
 Val Arg Leu Pro Asp Ala His Ala Val Asp Ala Asp Arg Tyr Gly Val
 1170 1175 1180
 55 His Pro Ala Leu Leu Asp Ala Val Leu His Pro Ile Ala Ser Leu Asp

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	1185	1190	1195	1200
	Pro Leu Gly Asp Gly Gly His Gly Leu Leu Pro Phe Ser Trp Thr Asp			
5	1205		1210	1215
	Val Gln Gly His Gly Ala Gly Gly His Ala Leu Arg Val Arg Val Ala			
	1220	1225		1230
10	Ala Val Asp Gly Gly Ala Val Ser Val Thr Ala Ala Asp His Ala Gly			
	1235	1240	1245	
	Asn Pro Val Leu Ser Ala Arg Ser Leu Ala Leu Arg Arg Ile Thr Ala			
	1250	1255	1260	
15	Asp Arg Leu Pro Ala Ala Pro Val Ala Pro Leu Tyr Arg Val Asp Trp			
	1265	1270	1275	1280
	Leu Pro Phe Pro Gly Pro Val Pro Val Ser Ala Gly Gly Arg Trp Ala			
	1285	1290	1295	
20	Val Val Gly Pro Glu Ala Glu Ala Thr Ala Ala Gly Leu Arg Ala Val			
	1300	1305	1310	
	Gly Leu Asp Val Arg Thr His Ala Leu Pro Leu Gly Glu Pro Leu Pro			
	1315	1320	1325	
25	Pro Gln Ala Gly Thr Asp Ala Glu Val Ile Ile Leu Asp Leu Thr Thr			
	1330	1335	1340	
	Thr Ala Ala Gly Arg Thr Ala Ser Asp Gly Gly Arg Leu Ser Leu Leu			
	1345	1350	1355	1360
30	Asp Glu Val Arg Ala Thr Val Arg Arg Thr Leu Glu Ala Val Gln Ala			
	1365	1370	1375	
	Arg Leu Ala Asp Thr Glu Thr Ala Pro Asp Val Asp Val Arg Thr Ala			
35	1380	1385	1390	
	Ala Arg Pro Arg Thr Ala Ala Arg Thr Ser Pro Arg Val Asp Thr Arg			
	1395	1400	1405	
40	Thr Gly Ala Arg Thr Ala Asp Gly Pro Arg Leu Val Val Leu Thr Arg			
	1410	1415	1420	
	Gly Ala Ala Gly Pro Glu Gly Gly Ala Ala Asp Pro Ala Gly Ala Ala			
	1425	1430	1435	1440
45	Val Trp Gly Leu Val Arg Val Ala Gln Ala Glu Gln Pro Gly Arg Phe			
	1445	1450	1455	
	Thr Leu Val Asp Val Asp Gly Thr Gln Ala Ser Leu Arg Ala Leu Pro			
	1460	1465	1470	
50	Gly Leu Leu Ala Thr Asp Ala Gly Gln Ser Ala Val Arg Asp Gly Arg			
	1475	1480	1485	
	Val Thr Val Pro Arg Leu Val Pro Val Ala Asp Pro Val Pro His Gly			
	1490	1495	1500	
55	Gly Gly Thr Ala Ala Asp Gly Thr Gly Ala Gly Glu Pro Ser Ala Thr			
	1505	1510	1515	1520

Leu Asp Pro Glu Gly Thr Val Leu Ile Thr Gly Gly Thr Gly Ala Leu
 1525 1530 1535
 5 Ala Ala Glu Thr Ala Arg His Leu Val Asp Arg His Lys Val Arg His
 1540 1545 1550
 Leu Leu Leu Val Gly Arg Arg Gly Pro Asp Ala Pro Gly Val Asp Arg
 1555 1560 1565
 10 Leu Val Ala Glu Leu Thr Glu Ser Gly Ala Glu Val Ala Val Arg Ala
 1570 1575 1580
 Cys Asp Val Thr Asp Arg Asp Ala Leu Arg Arg Leu Leu Asp Ala Leu
 1585 1590 1595 1600
 15 Pro Asp Glu His Pro Leu Thr Cys Val Val His Thr Ala Gly Val Leu
 1605 1610 1615
 Asp Asp Gly Val Leu Ser Ala Gln Thr Ala Glu Arg Ile Asp Thr Val
 20 1620 1625 1630
 Leu Arg Pro Lys Ala Asp Ala Ala Val His Leu Asp Glu Leu Thr Arg
 1635 1640 1645
 25 Glu Ile Gly Arg Val Pro Leu Val Leu Tyr Ser Ser Val Ser Ala Thr
 1650 1655 1660
 Leu Gly Ser Ala Gly Gln Ala Gly Tyr Ala Ala Ala Asn Ala Phe Met
 1665 1670 1675 1680
 30 Asp Ala Leu Ala Ala Arg Arg Cys Ala Ala Gly His Pro Ala Leu Ser
 1685 1690 1695
 Leu Gly Trp Gly Trp Trp Ser Gly Val Gly Leu Ala Thr Gly Leu Asp
 1700 1705 1710
 35 Gly Ala Asp Ala Ala Arg Val Arg Arg Ser Gly Leu Ala Pro Leu Asp
 1715 1720 1725
 Ala Gly Ala Ala Leu Asp Leu Leu Asp Arg Ala Leu Thr Arg Pro Glu
 1730 1735 1740
 40 Pro Ala Leu Leu Pro Val Arg Leu Asp Leu Arg Ala Ala Gly Ala
 1745 1750 1755 1760
 Thr Ala Leu Pro Glu Val Leu Arg Asp Leu Ala Gly Val Pro Ala Asp
 45 1765 1770 1775
 Ala Arg Ser Thr Pro Gly Ala Ala Ala Gly Thr Gly Asp Glu Asp Gly
 1780 1785 1790
 Ala Val Arg Pro Ala Pro Ala Asp Ala Ala Gly Thr Leu Ala
 50 1795 1800 1805
 Ala Arg Leu Ala Gly Arg Ser Ala Pro Glu Arg Thr Ala Leu Leu Leu
 1810 1815 1820
 55 Asp Leu Val Arg Thr Glu Val Ala Ala Val Leu Gly His Gly Asp Pro
 1825 1830 1835 1840

Ala Ala Ile Gly Ala Ala Arg Thr Phe Lys Asp Ala Gly Phe Asp Ser
 1845 1850 1855
 Leu Thr Ala Val Asp Leu Arg Asn Arg Leu Asn Thr Arg Thr Gly Leu
 5 1860 1865 1870
 Arg Leu Pro Ala Thr Leu Val Phe Asp His Pro Thr Pro Leu Ala Leu
 1875 1880 1885
 Ala Glu Leu Leu Leu Asp Gly Leu Glu Ala Ala Gly Pro Ala Glu Pro
 10 1890 1895 1900
 Ala Ala Glu Val Pro Asp Glu Ala Ala Gly Ala Glu Thr Leu Ser Gly
 1905 1910 1915 1920
 Val Ile Asp Arg Leu Glu Arg Ser Leu Ala Ala Thr Asp Asp Gly Asp
 15 1925 1930 1935
 Ala Arg Val Arg Ala Ala Arg Arg Leu Arg Gly Leu Leu Asp Ala Leu
 1940 1945 1950
 20 Pro Ala Gly Pro Gly Ala Ala Ser Gly Pro Asp Ala Gly Glu His Ala
 1955 1960 1965
 Pro Gly Arg Gly Asp Val Val Ile Asp Arg Leu Arg Ser Ala Ser Asp
 25 1970 1975 1980
 Asp Asp Leu Phe Asp Leu Leu Asp Ser Asp Phe Gln
 1985 1990 1995

30 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3724 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: unknown
 35 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
 40 Met Ser Ala Thr Asn Glu Glu Lys Leu Arg Glu Tyr Leu Arg Arg Ala
 1 5 10 15
 Met Ala Asp Leu His Ser Ala Arg Glu Arg Leu Arg Glu Val Glu Ser
 45 20 25 30
 Ala Ser Arg Glu Pro Ile Ala Ile Val Gly Met Ala Cys Arg Tyr Pro
 35 40 45
 Gly Gly Val Ala Ser Pro Glu Glu Leu Trp Asp Leu Val Ala Ala Gly
 50 55 60
 Thr Asp Ala Ile Ser Pro Phe Pro Val Asp Arg Gly Trp Asp Ala Glu
 65 70 75 80
 Gly Leu Tyr Asp Pro Glu Pro Gly Val Pro Gly Lys Ser Tyr Val Arg
 55 85 90 95

Glu Gly Gly Phe Leu His Ser Ala Ala Glu Phe Asp Ala Glu Phe Phe
 100 105 110
 Gly Ile Ser Pro Arg Glu Ala Ala Ala Met Asp Pro Gln Gln Arg Leu
 5 115 120 125
 Leu Leu Glu Thr Ser Trp Glu Ala Leu Glu Arg Ala Gly Ile Val Pro
 130 135 140
 Ala Ser Leu Arg Gly Thr Arg Thr Gly Val Phe Thr Gly Val Met Tyr
 10 145 150 155 160
 His Asp Tyr Gly Ser His Gln Val Gly Thr Ala Ala Asp Pro Ser Gly
 165 170 175
 Gln Leu Gly Leu Gly Thr Ala Gly Ser Val Ala Ser Gly Arg Val Ala
 15 180 185 190
 Tyr Thr Leu Gly Leu Gln Gly Pro Ala Val Thr Met Asp Thr Ala Cys
 195 200 205
 20 Ser Ser Ser Leu Val Ala Leu His Leu Ala Val Gln Ser Leu Arg Arg
 210 215 220
 Gly Glu Cys Asp Leu Ala Leu Ala Gly Gly Ala Thr Val Leu Ala Thr
 225 230 235 240
 25 Pro Thr Val Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Ala Asp
 245 250 255
 Gly Arg Cys Lys Ala Phe Ala Glu Gly Ala Asp Gly Thr Ala Trp Ala
 30 260 265 270
 Glu Gly Ala Gly Val Leu Leu Val Glu Arg Leu Ser Asp Ala Arg Arg
 275 280 285
 Asn Gly His Arg Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln
 35 290 295 300
 Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ala Gln Gln
 305 310 315 320
 Arg Val Ile Arg Asp Ala Leu Ala Asp Ala Gly Leu Thr Pro Ala Asp
 40 325 330 335
 Val Asp Ala Val Glu Ala His Gly Thr Gly Thr Pro Leu Gly Asp Pro
 340 345 350
 45 Ile Glu Ala Gly Ala Leu Met Ala Thr Tyr Gly Ser Glu Arg Val Gly
 355 360 365
 Asp Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Thr Gln
 370 375 380
 50 Ala Ala Ala Gly Ala Ala Gly Val Ile Lys Met Val Gln Ala Leu Arg
 385 390 395 400
 Gln Ser Glu Leu Pro Arg Thr Leu His Val Asp Ala Pro Ser Ala Lys
 55 405 410 415

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Val Glu Trp Asp Ala Gly Ala Val Gln Leu Leu Thr Gly Val Arg Pro
 420 425 430
 Trp Pro Arg Arg Glu His Arg Pro Arg Arg Ala Ala Val Ser Ala Phe
 5 435 440 445
 Gly Val Ser Gly Thr Asn Ala His Val Ile Ile Glu Glu Pro Pro Ala
 450 455 460
 Ala Gly Asp Thr Ser Pro Ala Gly Asp Thr Pro Glu Pro Gly Glu Ala
 10 465 470 475 480
 Thr Ala Ser Pro Ser Thr Ala Ala Gly Pro Ser Ser Pro Ser Ala Val
 485 490 495
 Ala Gly Pro Leu Ser Pro Ser Ser Pro Ala Val Val Trp Pro Leu Ser
 15 500 505 510
 Ala Glu Thr Ala Pro Ala Leu Arg Ala Gln Ala Ala Arg Leu Arg Ala
 515 520 525
 His Leu Glu Arg Leu Pro Gly Thr Ser Pro Thr Asp Ile Gly His Ala
 20 530 535 540
 Leu Ala Ala Glu Arg Ala Ala Leu Thr Arg Arg Val Val Leu Leu Gly
 545 550 555 560
 Asp Asp Gly Ala Pro Val Asp Ala Leu Ala Ala Leu Ala Ala Gly Glu
 25 565 570 575
 Thr Thr Pro Asp Ala Val His Gly Thr Ala Ala Asp Ile Arg Arg Val
 580 585 590
 Ala Phe Val Phe Pro Gly Gln Gly Ser Gln Trp Ala Gly Met Gly Ala
 30 595 600 605
 Glu Leu Leu Asp Thr Ala Pro Ala Phe Ala Ala Glu Leu Asp Arg Cys
 35 610 615 620
 Gln Gly Ala Leu Ser Pro Tyr Val Asp Trp Asn Leu Ala Asp Val Leu
 625 630 635 640
 Arg Gly Ala Pro Ala Ala Pro Gly Leu Asp Arg Val Asp Val Val Gln
 40 645 650 655
 Pro Ala Thr Phe Ala Val Met Val Gly Leu Ala Ala Leu Trp Arg Ser
 660 665 670
 Leu Gly Val Glu Pro Ala Ala Val Ile Gly His Ser Gln Gly Glu Ile
 45 675 680 685
 Ala Ala Ala Cys Val Ala Gly Ala Leu Ser Leu Glu Asp Ala Ala Arg
 690 695 700
 Ile Val Ala Leu Arg Ser Gln Val Ile Ala Arg Glu Leu Ala Gly Arg
 50 705 710 715 720
 Gly Gly Met Ala Ser Val Ala Leu Pro Ala Ala Glu Val Glu Ala Arg
 725 730 735
 55 Leu Ala Gly Gly Val Glu Ile Ala Ala Val Asn Gly Pro Gly Ser Thr

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	740	745	750
	Val Val Cys Gly Glu Pro Gly Ala Leu Glu Ala Leu Leu Val Thr Leu		
5	755	760	765
	Glu Ser Glu Gly Thr Arg Val Arg Arg Ile Asp Val Asp Tyr Ala Ser		
	770	775	780
10	His Ser His Tyr Val Glu Ser Ile Arg Ala Glu Leu Ala Thr Val Leu		
	785	790	795
	Gly Pro Val Arg Pro Arg Arg Gly Asp Val Pro Phe Tyr Ser Thr Val		
	805	810	815
	Glu Ala Ala Leu Leu Asp Thr Ala Thr Leu Asp Ala Asp Tyr Trp Tyr		
15	820	825	830
	Arg Asn Leu Arg Leu Pro Val Arg Phe Glu Pro Thr Val Arg Ala Met		
	835	840	845
20	Leu Asp Asp Gly Val Asp Ala Phe Val Glu Cys Ser Ala His Pro Val		
	850	855	860
	Leu Thr Val Gly Val Arg Gln Thr Val Glu Ser Ala Gly Gly Ala Val		
	865	870	875
	880		
25	Pro Ala Leu Ala Ser Leu Arg Arg Asp Glu Gly Gly Leu Arg Arg Phe		
	885	890	895
	Leu Thr Ser Ala Ala Glu Ala Gln Val Val Gly Val Pro Val Asp Trp		
	900	905	910
30	Ala Thr Leu Arg Pro Gly Ala Gly Arg Val Asp Leu Pro Thr Tyr Ala		
	915	920	925
	Phe Gln Arg Glu Arg His Trp Val Gly Pro Ala Arg Pro Asp Ser Ala		
	930	935	940
35	Ala Thr Ala Ala Thr Thr Gly Asp Asp Ala Pro Glu Pro Gly Asp Arg		
	945	950	955
	960		
	Leu Gly Tyr His Val Ala Trp Lys Gly Leu Arg Ser Thr Thr Gly Gly		
	965	970	975
40	Trp Arg Pro Gly Leu Arg Leu Leu Ile Val Pro Thr Gly Asp Gln Tyr		
	980	985	990
	Thr Ala Leu Ala Asp Thr Leu Glu Gln Ala Val Ala Ser Phe Gly Gly		
45	995	1000	1005
	Thr Val Arg Arg Val Ala Phe Asp Pro Ala Arg Thr Gly Arg Ala Glu		
	1010	1015	1020
50	Leu Phe Gly Leu Leu Glu Thr Glu Ile Asn Gly Asp Thr Ala Val Thr		
	1025	1030	1035
	1040		
	Gly Val Val Ser Leu Leu Gly Leu Cys Thr Asp Gly Arg Pro Asp His		
	1045	1050	1055
55	Pro Ala Val Pro Val Ala Val Thr Ala Thr Leu Ala Leu Val Gln Ala		
	1060	1065	1070

Leu Ala Asp Leu Gly Ser Thr Ala Pro Leu Trp Thr Val Thr Cys Gly
 1075 1080 1085
 5 Ala Val Ala Thr Ala Pro Asp Glu Leu Pro Cys Thr Ala Gly Ala Gln
 1090 1095 1100
 Leu Trp Gly Leu Gly Arg Val Ala Ala Leu Glu Leu Pro Glu Val Trp
 1105 1110 1115 1120
 10 Gly Gly Leu Ile Asp Leu Pro Ala Arg Pro Asp Ala Arg Val Leu Asp
 1125 1130 1135
 Arg Leu Ala Gly Val Leu Ala Glu Pro Gly Gly Glu Asp Gln Ile Ala
 1140 1145 1150
 15 Val Arg Met Ala Gly Val Phe Gly Arg Arg Val Leu Arg Asn Pro Ala
 1155 1160 1165
 Asp Ser Arg Pro Pro Ala Trp Arg Ala Arg Gly Thr Val Leu Ile Ala
 1170 1175 1180
 20 Gly Asp Leu Thr Thr Val Pro Gly Arg Leu Val Arg Ser Leu Leu Glu
 1185 1190 1195 1200
 Asp Gly Ala Asp Arg Val Val Leu Ala Gly Pro Asp Ala Pro Ala Gln
 1205 1210 1215
 25 Ala Ala Ala Ala Gly Leu Thr Gly Val Ser Leu Val Pro Val Arg Cys
 1220 1225 1230
 Asp Val Thr Asp Arg Ala Ala Leu Ala Ala Leu Leu Asp Glu His Ala
 1235 1240 1245
 30 Pro Thr Val Ala Val His Ala Pro Pro Leu Val Pro Leu Ala Pro Leu
 1250 1255 1260
 Arg Glu Thr Ala Pro Gly Asp Ile Ala Ala Leu Ala Ala Lys Thr
 1265 1270 1275 1280
 35 Thr Ala Ala Gly His Leu Val Asp Leu Ala Pro Ala Ala Gly Leu Asp
 1285 1290 1295
 Ala Leu Val Leu Phe Ser Ser Val Ser Gly Val Trp Gly Gly Ala Ala
 1300 1305 1310
 40 Gln Gly Gly Tyr Ala Ala Ala Ser Ala His Leu Asp Ala Leu Ala Glu
 1315 1320 1325
 Arg Ala Arg Ala Ala Gly Val Pro Ala Phe Ser Val Ala Trp Ser Pro
 1330 1335 1340
 Trp Ala Gly Gly Thr Pro Ala Asp Gly Ala Glu Ala Glu Phe Leu Ser
 1345 1350 1355 1360
 45 Arg Arg Gly Leu Ala Pro Leu Asp Pro Asp Gln Ala Val Arg Thr Leu
 1365 1370 1375
 Arg Arg Met Leu Glu Arg Gly Ser Ala Cys Gly Ala Val Ala Asp Val
 1380 1385 1390
 50
 55

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Glu Trp Ser Arg Phe Ala Ala Ser Tyr Thr Trp Val Arg Pro Ala Val
 1395 1400 1405
 Leu Phe Asp Asp Ile Pro Asp Val Gln Arg Leu Arg Ala Ala Glu Leu
 5 1410 1415 1420
 Ala Pro Ser Thr Gly Asp Ser Thr Thr Ser Glu Leu Val Arg Glu Leu
 1425 1430 1435 1440
 Thr Ala Gln Ser Gly His Lys Arg His Ala Thr Leu Leu Arg Leu Val
 10 1445 1450 1455
 Arg Ala His Ala Ala Ala Val Leu Gly Gln Ser Ser Gly Asp Ala Val
 1460 1465 1470
 Ser Ser Ala Arg Ala Phe Arg Asp Leu Gly Phe Asp Ser Leu Thr Ala
 15 1475 1480 1485
 Leu Glu Leu Arg Asp Arg Leu Ser Thr Ser Thr Gly Leu Lys Leu Pro
 1490 1495 1500
 20 Thr Ser Leu Val Phe Asp His Ser Ser Pro Ala Ala Leu Ala Arg His
 1505 1510 1515 1520
 Leu Gly Glu Glu Leu Leu Gly Arg Asn Asp Thr Ala Asp Arg Ala Gly
 1525 1530 1535
 Pro Asp Thr Pro Val Arg Thr Asp Glu Pro Ile Ala Ile Ile Gly Met
 25 1540 1545 1550
 Ala Cys Arg Leu Pro Gly Gly Val Gln Ser Pro Glu Asp Leu Trp Asp
 1555 1560 1565
 30 Leu Leu Thr Gly Gly Thr Asp Ala Ile Thr Pro Phe Pro Thr Asn Arg
 1570 1575 1580
 Gly Trp Asp Asn Glu Thr Leu Tyr Asp Pro Asp Pro Asp Ser Pro Gly
 35 1585 1590 1595 1600
 His His Thr Tyr Val Arg Glu Gly Gly Phe Leu His Asp Ala Ala Glu
 1605 1610 1615
 Phe Asp Pro Gly Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met
 40 1620 1625 1630
 Asp Pro Gln Gln Arg Leu Ile Leu Glu Thr Ser Trp Glu Ser Phe Glu
 1635 1640 1645
 Arg Ala Gly Ile Asp Pro Val Glu Leu Arg Gly Ser Arg Thr Gly Val
 45 1650 1655 1660
 Phe Val Gly Thr Asn Gly Gln His Tyr Val Pro Leu Leu Gln Asp Gly
 1665 1670 1675 1680
 Asp Glu Asn Phe Asp Gly Tyr Ile Ala Thr Gly Asn Ser Ala Ser Val
 50 1685 1690 1695
 Met Ser Gly Arg Leu Ser Tyr Val Phe Gly Leu Glu Gly Pro Ala Val
 1700 1705 1710
 55 Thr Val Asp Thr Ala Cys Ser Ala Ser Leu Ala Ala Leu His Leu Ala

	1715	1720	1725
	Val Gln Ser Leu Arg Arg Gly Glu Cys Asp Tyr Ala Leu Ala Gly Gly		
5	1730	1735	1740
	Ala Thr Val Met Ser Thr Pro Glu Met Leu Val Glu Phe Ala Arg Gln		
	1745	1750	1755
	Arg Ala Val Ser Pro Asp Gly Arg Ser Lys Ala Phe Ala Glu Ala Ala		
10	1765	1770	1775
	Asp Gly Val Gly Leu Ala Glu Gly Ala Gly Met Leu Leu Val Glu Arg		
	1780	1785	1790
15	Leu Ser Glu Ala Gln Lys Lys Gly His Pro Val Leu Ala Val Val Arg		
	1795	1800	1805
	Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro		
	1810	1815	1820
20	Ser Gly Pro Ala Gln Gln Arg Val Ile Arg Glu Ala Leu Ala Asp Ala		
	1825	1830	1835
	Gly Leu Thr Pro Ala Asp Val Asp Ala Val Glu Ala His Gly Thr Gly		
	1845	1850	1855
25	Thr Pro Leu Gly Asp Pro Ile Glu Ala Gly Ala Leu Leu Ala Thr Tyr		
	1860	1865	1870
	Gly Arg Asp Arg Arg Asp Gly Pro Leu Trp Leu Gly Ser Leu Lys Ser		
	1875	1880	1885
30	Asn Ile Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys		
	1890	1895	1900
	Met Val Leu Ala Leu Arg His Gly Glu Leu Pro Arg Thr Leu His Ala		
	1905	1910	1915
	1920		
35	Ser Thr Ala Ser Ser Arg Ile Asp Trp Asp Ala Gly Ala Val Glu Leu		
	1925	1930	1935
	Leu Asp Glu Ala Arg Pro Trp Leu Gln Arg Ala Glu Gly Pro Arg Arg		
	1940	1945	1950
40	Ala Gly Ile Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His Leu Val		
	1955	1960	1965
	Ile Glu Glu Pro Pro Glu Pro Thr Ala Pro Glu Leu Leu Ala Pro Glu		
45	1970	1975	1980
	Pro Ala Ala Asp Gly Asp Val Trp Ser Glu Glu Trp Trp His Glu Val		
	1985	1990	1995
	2000		
50	Thr Val Pro Leu Met Met Ser Ala His Asn Glu Ala Ala Leu Arg Asp		
	2005	2010	2015
	Gln Ala Arg Arg Leu Arg Ala Asp Leu Leu Ala His Pro Glu Leu His		
	2020	2025	2030
55	Pro Ala Asp Val Gly Tyr Thr Leu Ile Thr Thr Arg Thr Arg Phe Glu		
	2035	2040	2045

Gln Arg Ala Ala Val Val Gly Glu Asn Phe Thr Glu Leu Ile Ala Ala
 2050 2055 2060
 5 Leu Asp Asp Leu Val Glu Gly Arg Pro His Pro Leu Val Leu Arg Gly
 2065 2070 2075 2080
 Thr Ala Gly Thr Ser Asp Gln Val Val Phe Val Phe Pro Gly Gln Gly
 2085 2090 2095
 10 Ser Gln Trp Pro Glu Met Ala Asp Gly Leu Leu Ala Arg Ser Ser Gly
 2100 2105 2110
 Ser Gly Ser Phe Leu Glu Thr Ala Arg Ala Cys Asp Leu Ala Leu Arg
 2115 2120 2125
 15 Pro His Leu Gly Trp Ser Val Leu Asp Val Leu Arg Arg Glu Pro Gly
 2130 2135 2140
 Ala Pro Ser Leu Asp Arg Val Asp Val Val Gln Pro Val Leu Phe Thr
 2145 2150 2155 2160
 Met Met Val Ser Leu Ala Glu Thr Trp Arg Ser Leu Gly Val Glu Pro
 2165 2170 2175
 25 Ala Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala Tyr Val
 2180 2185 2190
 Ala Gly Ala Leu Thr Leu Asp Asp Ala Ala Arg Ile Val Ala Leu Arg
 2195 2200 2205
 30 Ser Gln Ala Trp Leu Arg Leu Ala Gly Lys Gly Gly Met Val Ala Val
 2210 2215 2220
 Thr Leu Ser Glu Arg Asp Leu Arg Pro Arg Leu Glu Pro Trp Ser Asp
 2225 2230 2235 2240
 Arg Leu Ala Val Ala Ala Val Asn Gly Pro Glu Thr Cys Ala Val Ser
 2245 2250 2255
 35 Gly Asp Pro Asp Ala Leu Ala Glu Leu Val Ala Glu Leu Gly Ala Glu
 2260 2265 2270
 Gly Val His Ala Arg Pro Ile Pro Gly Val Asp Thr Ala Gly His Ser
 2275 2280 2285
 40 Pro Gln Val Asp Thr Leu Glu Ala His Leu Arg Lys Val Leu Ala Pro
 2290 2295 2300
 45 Val Ala Pro Arg Thr Ser Asp Ile Pro Phe Tyr Ser Thr Val Thr Gly
 2305 2310 2315 2320
 Gly Leu Ile Asp Thr Ala Glu Leu Asp Ala Asp Tyr Trp Tyr Arg Asn
 2325 2330 2335
 50 Met Arg Glu Pro Val Glu Phe Glu Gln Ala Thr Arg Ala Leu Ile Ala
 2340 2345 2350
 Asp Gly His Asp Val Phe Leu Glu Ser Ser Pro His Pro Met Leu Ala
 55 2355 2360 2365

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Val Ser Leu Gln Glu Thr Ile Ser Asp Ala Gly Ser Pro Ala Ala Val
 2370 2375 2380
 5 Leu Gly Thr Leu Arg Arg Gly Gln Gly Gly Pro Arg Trp Leu Gly Val
 2385 2390 2395 2400
 Ala Leu Cys Arg Ala Tyr Thr His Gly Leu Glu Ile Asp Ala Glu Ala
 2405 2410 2415
 10 Ile Phe Gly Pro Asp Ser Arg Gln Val Glu Leu Pro Thr Tyr Pro Phe
 2420 2425 2430
 Gln Arg Glu Arg Tyr Trp Tyr Ser Pro Gly His Arg Gly Asp Asp Pro
 2435 2440 2445
 15 Ala Ser Leu Gly Leu Asp Ala Val Asp His Pro Leu Leu Gly Ser Gly
 2450 2455 2460
 Val Glu Leu Pro Glu Ser Gly Asp Arg Met Tyr Thr Ala Arg Leu Gly
 2465 2470 2475 2480
 20 Ala Asp Thr Thr Pro Trp Leu Ala Asp His Ala Leu Leu Gly Ser Pro
 2485 2490 2495
 Leu Leu Pro Gly Ala Ala Phe Ala Asp Leu Ala Leu Trp Ala Gly Arg
 2500 2505 2510
 25 Gln Ala Gly Thr Gly Arg Val Glu Glu Leu Thr Leu Ala Ala Pro Leu
 2515 2520 2525
 Val Leu Pro Gly Ser Gly Gly Val Arg Leu Arg Leu Asn Val Gly Ala
 30 2530 2535 2540
 Pro Gly Thr Asp Asp Ala Arg Arg Phe Ala Val His Ala Arg Ala Glu
 2545 2550 2555 2560
 35 Gly Ala Thr Asp Trp Thr Leu His Ala Glu Gly Leu Leu Thr Ala Gln
 2565 2570 2575
 Asp Thr Ala Asp Ala Pro Asp Ala Ser Ala Ala Thr Pro Pro Pro Gly
 2580 2585 2590
 Ala Glu Gln Leu Asp Ile Gly Asp Phe Tyr Gln Arg Phe Ser Glu Leu
 40 2595 2600 2605
 Gly Tyr Gly Tyr Gly Pro Phe Phe Arg Gly Leu Val Ser Ala His Arg
 2610 2615 2620
 Cys Gly Pro Asp Ile His Ala Glu Val Ala Leu Pro Val Gln Ala Gln
 45 2625 2630 2635 2640
 Gly Asp Ala Ala Arg Phe Gly Ile His Pro Ala Leu Leu Asp Ala Ala
 2645 2650 2655
 50 Leu Gln Thr Met Ser Leu Gly Gly Phe Phe Pro Glu Asp Gly Arg Val
 2660 2665 2670
 Arg Met Pro Phe Ala Leu Arg Gly Val Arg Leu Tyr Arg Ala Gly Ala
 2675 2680 2685
 55 Asp Arg Leu His Val Arg Val Ser Pro Val Ser Glu Asp Ala Val Arg

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	2690	2695	2700
	Ile Arg Cys Ala Asp Gly Glu Gly Arg Pro Val Ala Glu Ile Glu Ser		
5	2705	2710	2715
	Phe Ile Met Arg Pro Val Asp Pro Gly Gln Leu Leu Gly Gly Arg Pro		
	2725	2730	2735
10	Val Gly Ala Asp Ala Leu Phe Arg Ile Ala Trp Arg Glu Leu Ala Ala		
	2740	2745	2750
	Gly Pro Gly Thr Arg Thr Gly Asp Gly Thr Pro Pro Pro Val Arg Trp		
	2755	2760	2765
15	Val Leu Ala Gly Pro Asp Ala Leu Gly Leu Ala Glu Ala Ala Asp Ala		
	2770	2775	2780
	His Leu Pro Ala Val Pro Gly Pro Asp Gly Ala Leu Pro Ser Pro Thr		
	2785	2790	2795
20	Gly Arg Pro Ala Pro Asp Ala Val Val Phe Ala Val Arg Ala Gly Thr		
	2805	2810	2815
	Gly Asp Val Ala Ala Asp Ala His Thr Val Ala Cys Arg Val Leu Asp		
	2820	2825	2830
25	Leu Val Gln Arg Arg Leu Ala Ala Pro Glu Gly Pro Asp Gly Ala Arg		
	2835	2840	2845
	Leu Val Val Ala Thr Arg Gly Ala Val Ala Val Arg Asp Asp Ala Glu		
	2850	2855	2860
30	Val Asp Asp Pro Ala Ala Ala Ala Trp Gly Leu Leu Arg Ser Ala		
	2865	2870	2875
	Gln Ala Glu Glu Pro Gly Arg Phe Leu Leu Val Asp Leu Asp Asp Asp		
35	2885	2890	2895
	Pro Ala Ser Ala Arg Ala Leu Thr Asp Ala Leu Ala Ser Gly Glu Pro		
	2900	2905	2910
40	Gln Thr Ala Val Arg Ala Gly Thr Val Tyr Val Pro Arg Leu Glu Arg		
	2915	2920	2925
	Ala Ala Asp Arg Thr Asp Gly Pro Leu Thr Pro Pro Asp Asp Gly Ala		
	2930	2935	2940
45	Trp Arg Leu Gly Arg Gly Thr Asp Leu Thr Leu Asp Gly Leu Ala Leu		
	2945	2950	2955
	Val Pro Ala Pro Asp Ala Glu Ala Pro Leu Glu Pro Gly Gln Val Arg		
	2965	2970	2975
50	Val Ala Val Arg Ala Ala Gly Val Asn Phe Arg Asp Ala Leu Ile Ala		
	2980	2985	2990
	Leu Gly Met Tyr Pro Gly Glu Ala Glu Met Gly Thr Glu Gly Ala Gly		
	2995	3000	3005
55	Thr Val Val Glu Val Gly Pro Gly Val Thr Gly Val Ala Val Gly Asp		
	3010	3015	3020

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Arg Val Leu Gly Leu Trp Asp Gly Gly Leu Gly Pro Leu Cys Val Ala
 3025 3030 3035 3040
 5 Asp His Arg Leu Leu Ala Pro Val Pro Asp Gly Trp Ser Tyr Ala Gln
 3045 3050 3055
 Ala Ala Ser Val Pro Ala Val Phe Leu Ser Ala Tyr Tyr Gly Leu Val
 3060 3065 3070
 10 Thr Leu Ala Gly Leu Arg Pro Gly Glu Arg Val Leu Val His Ala Ala
 3075 3080 3085
 Ala Gly Gly Val Gly Met Ala Ala Val Gln Ile Ala Arg His Leu Gly
 15 3090 3095 3100
 Ala Glu Val Leu Ala Thr Ala Ser Pro Gly Lys Trp Asp Ala Leu Arg
 3105 3110 3115 3120
 Ala Met Gly Ile Thr Asp Asp His Leu Ala Ser Ser Arg Thr Leu Asp
 20 3125 3130 3135
 Phe Ala Thr Ala Phe Thr Gly Ala Asp Gly Thr Ser Arg Ala Asp Val
 3140 3145 3150
 Val Leu Asn Ser Leu Thr Lys Glu Phe Val Asp Ala Ser Leu Gly Leu
 25 3155 3160 3165
 Leu Arg Pro Gly Gly Arg Phe Leu Glu Leu Gly Lys Thr Asp Val Arg
 3170 3175 3180
 30 Asp Pro Glu Arg Ile Ala Ala Glu His Pro Gly Val Arg Tyr Arg Ala
 3185 3190 3195 3200
 Phe Asp Leu Asn Glu Ala Gly Pro Asp Ala Leu Gly Arg Leu Leu Arg
 3205 3210 3215
 35 Glu Leu Met Asp Leu Phe Ala Ala Gly Val Leu His Pro Leu Pro Val
 3220 3225 3230
 Val Thr His Asp Val Arg Arg Ala Ala Asp Ala Leu Arg Thr Ile Ser
 3235 3240 3245
 40 Gln Ala Arg His Thr Gly Lys Leu Val Leu Thr Met Pro Pro Ala Trp
 3250 3255 3260
 His Pro Tyr Gly Thr Val Leu Val Thr Gly Gly Thr Gly Ala Leu Gly
 45 3265 3270 3275 3280
 Ser Arg Ile Ala Arg His Leu Ala Ser Arg His Gly Val Arg Arg Leu
 3285 3290 3295
 Leu Ile Ala Ala Arg Arg Gly Pro Asp Gly Glu Gly Ala Ala Glu Leu
 50 3300 3305 3310
 Val Ala Asp Leu Ala Ala Leu Gly Ala Ser Ala Thr Val Val Ala Cys
 3315 3320 3325
 Asp Val Ser Asp Ala Asp Ala Val Arg Gly Leu Leu Ala Gly Ile Pro
 55 3330 3335 3340

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Ala Asp His Pro Leu Thr Ala Val Val His Ser Thr Gly Val Leu Asp
 3345 3350 3355 3360
 5 Asp Gly Val Leu Pro Gly Leu Thr Pro Glu Arg Met Arg Arg Val Leu
 3365 3370 3375
 Arg Pro Lys Val Glu Ala Ala Val His Leu Asp Glu Leu Thr Arg Asp
 3380 3385 3390
 10 Leu Asp Leu Ser Ala Phe Val Leu Phe Ser Ser Ser Ala Gly Leu Leu
 3395 3400 3405
 Gly Ser Pro Ala Gln Gly Asn Tyr Ala Ala Asn Ala Thr Leu Asp
 3410 3415 3420
 15 Ala Leu Ala Ala Arg Arg Arg Ser Leu Gly Leu Pro Ser Val Ser Leu
 3425 3430 3435 3440
 Ala Trp Gly Leu Trp Ser Asp Thr Ser Arg Met Ala His Ala Leu Asp
 3445 3450 3455
 20 Gln Glu Ser Leu Gln Arg Arg Phe Ala Arg Ser Gly Phe Pro Pro Leu
 3460 3465 3470
 Ser Ala Thr Leu Gly Ala Ala Leu Phe Asp Ala Ala Leu Arg Val Asp
 3475 3480 3485
 25 Glu Ala Val Gln Val Pro Met Arg Phe Asp Pro Ala Ala Leu Arg Ala
 3490 3495 3500
 Thr Gly Ser Val Pro Ala Leu Leu Ser Asp Leu Val Gly Ser Ala Pro
 3505 3510 3515 3520
 30 Ala Thr Gly Ser Ala Ala Pro Ala Ser Gly Pro Leu Pro Ala Pro Asp
 3525 3530 3535
 Ala Gly Thr Val Gly Glu Pro Leu Ala Glu Arg Leu Ala Gly Leu Ser
 3540 3545 3550
 35 Ala Glu Glu Arg His Asp Arg Leu Leu Gly Leu Val Gly Glu His Val
 3555 3560 3565
 40 Ala Ala Val Leu Gly His Gly Ser Ala Ala Glu Val Arg Pro Asp Arg
 3570 3575 3580
 Pro Phe Arg Glu Val Gly Phe Asp Ser Leu Thr Ala Val Glu Leu Arg
 3585 3590 3595 3600
 45 Asn Arg Met Ala Ala Val Thr Gly Val Arg Leu Pro Ala Thr Leu Val
 3605 3610 3615
 Phe Asp His Pro Thr Pro Ala Ala Leu Ser Ser His Leu Asp Gly Leu
 3620 3625 3630
 50 Leu Ala Pro Ala Gln Pro Val Thr Thr Thr Pro Leu Leu Ser Glu Leu
 3635 3640 3645
 Asp Arg Ile Glu Glu Ala Leu Ala Leu Thr Pro Glu His Leu Ala
 3650 3655 3660
 55 Glu Leu Ala Pro Ala Pro Asp Asp Arg Ala Glu Val Ala Leu Arg Leu

3665	3670	3675	3680
Asp Ala Leu Ala Asp Arg Trp Arg Ala Leu His Asp Gly Ala Pro Gly			
3685	3690	3695	
Ala Asp Asp Asp Ile Thr Asp Val Leu Ser Ser Ala Asp Asp Asp Glu			
3700	3705	3710	
Ile Phe Ala Phe Ile Asp Glu Arg Tyr Gly Thr Ser			
3715	3720		

5

10

(2) INFORMATION FOR SEQ ID NO:11:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1580 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

- 20 (ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Asn Glu Glu Lys Leu Arg Ala Tyr Leu Lys Arg Val Thr Gly
1 5 10 15

25

Glu Leu His Arg Ala Thr Glu Gln Leu Arg Ala Leu Asp Arg Arg Ala
20 25 30

30

His Glu Pro Ile Ala Ile Val Gly Ala Ala Cys Arg Leu Pro Gly Gly
35 40 45

Val Glu Ser Pro Asp Asp Leu Trp Glu Leu Leu His Ala Gly Ala Asp
50 55 60

35

Ala Val Gly Pro Ala Pro Ala Asp Arg Gly Trp Asp Val Glu Gly Arg
65 70 75 80

Tyr Ser Pro Asp Pro Asp Thr Pro Gly Thr Ser Tyr Cys Arg Glu Gly
85 90 95

40

Gly Phe Val Gln Gly Ala Asp Arg Phe Asp Pro Ala Leu Phe Gly Ile
100 105 110

Ser Pro Asn Glu Ala Leu Thr Met Asp Pro Gln Gln Arg Leu Leu Leu
115 120 125

45

Glu Thr Ser Trp Glu Ala Leu Glu Arg Ala Gly Leu Asp Pro Gln Ser
130 135 140

Leu Ala Gly Ser Arg Thr Gly Val Phe Ala Gly Ala Trp Glu Ser Gly
145 150 155 160

50

Tyr Gln Lys Gly Val Glu Gly Leu Glu Ala Asp Leu Glu Ala Gln Leu
165 170 175

Leu Ala Gly Ile Val Ser Phe Thr Ala Gly Arg Val Ala Tyr Ala Leu
180 185 190

55

Gly Leu Glu Gly Pro Ala Leu Thr Ile Asp Thr Ala Cys Ser Ser Ser

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	195	200	205	
	Leu Val Ala Leu His Leu Ala Val Gln Ser Leu Arg Arg Gly Glu Cys			
5	210	215	220	
	Asp Leu Ala Leu Ala Gly Gly Ala Thr Val Ile Ala Asp Phe Ala Leu			
	225	230	235	240
	Phe Thr Gln Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg Cys			
10	245	250	255	
	Lys Ala Phe Gly Glu Thr Ala Asp Gly Phe Gly Pro Ala Glu Gly Ala			
	260	265	270	
15	Gly Met Leu Leu Val Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly His			
	275	280	285	
	Pro Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly Ala			
	290	295	300	
20	Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ala Gln Gln Arg Val Ile			
	305	310	315	320
	Arg Glu Ala Leu Ala Asp Ala Gly Leu Thr Pro Ala Asp Val Asp Ala			
	325	330	335	
25	Val Glu Ala His Gly Thr Gly Thr Pro Leu Gly Asp Pro Ile Glu Ala			
	340	345	350	
	Gly Ala Leu Met Ala Thr Tyr Gly His Glu Arg Thr Gly Asp Pro Leu			
	355	360	365	
30	Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Thr Gln Ala Ala Ala			
	370	375	380	
	Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Leu Arg His Gly Glu			
35	385	390	395	400
	Leu Pro Arg Thr Leu His Ala Ser Thr Ala Ser Ser Arg Ile Glu Trp			
	405	410	415	
40	Asp Ala Gly Ala Val Glu Leu Leu Asp Glu Ala Arg Pro Trp Pro Arg			
	420	425	430	
	Arg Ala Glu Gly Pro Arg Arg Ala Gly Ile Ser Ser Phe Gly Ile Ser			
	435	440	445	
45	Gly Thr Asn Ala His Leu Val Ile Glu Glu Glu Pro Pro Ala Arg Pro			
	450	455	460	
	Glu Pro Glu Glu Ala Ala Gln Pro Pro Ala Pro Ala Thr Thr Val Leu			
	465	470	475	480
50	Pro Leu Ser Ala Ala Gly Ala Arg Ser Leu Arg Glu Gln Ala Arg Arg			
	485	490	495	
	Leu Ala Ala His Leu Ala Gly His Glu Glu Ile Thr Ala Ala Asp Ala			
	500	505	510	
55	Ala Arg Ser Ala Ala Thr Thr Arg Ala Ala Leu Ser His Arg Ala Ser			

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	515	520	525
	Val Leu Ala Asp Asp Arg Arg Ala Leu Ile Asp Arg Leu Thr Ala Leu		
	530	535	540
5	Ala Glu Asp Arg Lys Asp Pro Gly Val Thr Val Gly Glu Ala Gly Ser		
	545	550	555
	Gly Arg Pro Pro Val Phe Val Phe Pro Gly Gln Gly Ser Gln Trp Thr		
	565	570	575
10	Gly Met Gly Ala Glu Leu Leu Asp Arg Ala Pro Val Phe Arg Ala Lys		
	580	585	590
	Ala Glu Glu Cys Ala Arg Ala Leu Ala Ala His Leu Asp Trp Ser Val		
	595	600	605
15	Leu Asp Val Leu Arg Asp Ala Pro Gly Ala Pro Pro Ile Asp Arg Ala		
	610	615	620
	Asp Val Val Gln Pro Thr Leu Phe Thr Met Met Val Ser Leu Ala Ala		
20	625	630	635
	Leu Trp Glu Ser His Gly Val Arg Pro Ala Ala Val Val Gly His Ser		
	645	650	655
25	Gln Gly Glu Ile Ala Ala Ala His Ala Ala Gly Ala Leu Ser Leu Asp		
	660	665	670
	Asp Ala Ala Arg Val Ile Ala Glu Arg Ser Arg Leu Trp Lys Arg Leu		
	675	680	685
30	Ala Gly Asn Gly Met Leu Ser Val Met Ala Pro Ala Asp Arg Val		
	690	695	700
	Arg Glu Leu Met Glu Pro Trp Ala Glu Arg Met Ser Val Ala Ala Val		
	705	710	715
	720		
35	Asn Gly Pro Ala Ser Val Thr Val Ala Gly Asp Ala Arg Ala Leu Glu		
	725	730	735
	Glu Phe Gly Gly Arg Leu Ser Ala Ala Gly Val Leu Arg Trp Pro Leu		
	740	745	750
40	Ala Gly Val Asp Phe Ala Gly His Ser Pro Gln Val Glu Gln Phe Arg		
	755	760	765
	Ala Glu Leu Leu Asp Thr Leu Gly Thr Val Arg Pro Thr Ala Ala Arg		
45	770	775	780
	Leu Pro Phe Phe Ser Thr Val Thr Ala Ala Ala His Glu Pro Glu Gly		
	785	790	795
	800		
50	Leu Asp Ala Ala Tyr Trp Tyr Arg Asn Met Arg Glu Pro Val Glu Phe		
	805	810	815
	Ala Ser Thr Leu Arg Thr Leu Leu Arg Glu Gly His Arg Thr Phe Val		
	820	825	830
55	Glu Met Gly Pro His Pro Leu Leu Gly Ala Ala Ile Asp Glu Val Ala		
	835	840	845

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Glu Ala Glu Gly Val His Ala Thr Ala Leu Ala Thr Leu His Arg Gly
 850 855 860
 5 Ser Gly Gly Leu Asp Arg Phe Arg Ser Ser Val Gly Ala Ala Phe Ala
 865 870 875 880
 His Gly Val Arg Val Asp Trp Asp Ala Leu Phe Glu Gly Ser Gly Ala
 885 890 895
 10 Arg Arg Val Pro Leu Pro Thr Tyr Ala Phe Ser Arg Asp Arg Tyr Trp
 900 905 910
 Leu Pro Thr Ala Ile Gly Arg Arg Ala Val Glu Ala Ala Pro Val Asp
 915 920 925
 15 Ala Ser Ala Pro Gly Arg Tyr Arg Val Thr Trp Thr Pro Val Ala Ser
 930 935 940
 Asp Asp Ser Gly Arg Pro Ser Gly Arg Trp Leu Leu Val Gln Thr Pro
 945 950 955 960
 20 Gly Thr Ala Pro Asp Glu Ala Asp Thr Ala Ala Ser Ala Leu Gly Ala
 965 970 975
 Ala Gly Val Val Val Glu Arg Cys Leu Leu Asp Pro Thr Glu Ala Ala
 980 985 990
 25 Arg Val Thr Leu Thr Glu Arg Leu Ala Glu Leu Asp Ala Gln Pro Glu
 995 1000 1005
 Gly Leu Ala Gly Val Leu Val Leu Pro Gly Arg Pro Gln Ser Thr Ala
 1010 1015 1020
 30 Pro Ala Asp Ala Ser Pro Leu Asp Pro Gly Thr Ala Ala Val Leu Leu
 1025 1030 1035 1040
 Val Val Gln Ala Val Pro Asp Ala Ala Pro Lys Ala Arg Ile Trp Val
 1045 1050 1055
 35 Val Thr Arg Gly Ala Val Ala Val Gly Ser Gly Glu Val Pro Cys Ala
 1060 1065 1070
 40 Val Gly Ala Arg Val Trp Gly Leu Gly Arg Val Ala Ala Leu Glu Val
 1075 1080 1085
 Pro Val Gln Trp Gly Gly Leu Val Asp Val Ala Val Gly Ala Gly Val
 1090 1095 1100
 45 Arg Glu Trp Arg Arg Val Val Gly Val Val Ala Gly Gly Glu Asp
 1105 1110 1115 1120
 Gln Val Ala Val Arg Gly Gly Val Phe Gly Arg Arg Leu Val Gly
 1125 1130 1135
 50 Val Gly Val Arg Gly Gly Ser Gly Val Trp Arg Ala Arg Gly Cys Val
 1140 1145 1150
 Val Val Thr Gly Gly Leu Gly Gly Val Gly Gly His Val Ala Arg Trp
 1155 1160 1165

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Leu Ala Arg Ser Gly Ala Glu His Val Val Leu Ala Gly Arg Arg Gly
 1170 1175 1180
 Gly Gly Val Val Gly Ala Val Glu Leu Glu Arg Glu Leu Val Gly Leu
 5 1185 1190 1195 1200
 Gly Ala Lys Val Thr Phe Val Ser Cys Asp Val Gly Asp Arg Ala Ser
 1205 1210 1215
 Met Val Gly Leu Leu Gly Val Val Glu Gly Leu Gly Val Pro Leu Arg
 10 1220 1225 1230
 Gly Val Phe His Ala Ala Gly Val Ala Gln Val Ser Gly Leu Gly Glu
 1235 1240 1245
 Val Ser Leu Ala Glu Ala Gly Gly Val Leu Gly Gly Lys Ala Val Gly
 15 1250 1255 1260
 Ala Glu Leu Leu Asp Glu Leu Thr Ala Gly Val Glu Leu Asp Ala Phe
 1265 1270 1275 1280
 Val Leu Phe Ser Ser Gly Ala Gly Val Trp Gly Ser Gly Gly Gln Ser
 20 1285 1290 1295
 Val Tyr Ala Ala Ala Asn Ala His Leu Asp Ala Leu Ala Glu Arg Arg
 1300 1305 1310
 Arg Ala Gln Gly Arg Pro Ala Thr Ser Val Ala Trp Gly Leu Trp Gly
 25 1315 1320 1325
 Gly Glu Gly Met Gly Ala Asp Glu Gly Val Thr Glu Phe Tyr Ala Glu
 1330 1335 1340
 Arg Gly Leu Ala Pro Met Arg Pro Glu Ser Gly Ile Glu Ala Leu His
 30 1345 1350 1355 1360
 Thr Ala Leu Asn Glu Gly Asp Thr Cys Val Thr Val Ala Asp Ile Asp
 1365 1370 1375
 Trp Glu His Phe Val Thr Gly Phe Thr Ala Tyr Arg Pro Ser Pro Leu
 35 1380 1385 1390
 Ile Ser Asp Ile Pro Gln Val Arg Ala Leu Arg Thr Pro Glu Pro Thr
 40 1395 1400 1405
 Val Asp Ala Ser Asp Gly Leu Arg Arg Arg Val Asp Ala Ala Leu Thr
 1410 1415 1420
 Pro Arg Glu Arg Thr Lys Val Leu Val Asp Leu Val Arg Thr Val Ala
 45 1425 1430 1435 1440
 Ala Glu Val Leu Gly His Asp Gly Ile Gly Gly Ile Gly His Asp Val
 1445 1450 1455
 Ala Phe Arg Asp Leu Gly Phe Asp Ser Leu Ala Ala Val Arg Met Arg
 50 1460 1465 1470
 Gly Arg Leu Ala Glu Ala Thr Gly Leu Val Leu Pro Ala Thr Val Ile
 1475 1480 1485
 55 Phe Asp His Pro Thr Val Asp Arg Leu Gly Gly Ala Leu Leu Glu Arg

1490 1495 1500

Leu Ser Ala Asp Glu Pro Ala Pro Gly Gly Ala Pro Glu Pro Ala Gly
 1505 1510 1515 1520

5

Gly Arg Pro Ala Thr Pro Pro Pro Ala Pro Glu Pro Ala Val His Asp
 1525 1530 1535

10

Ala Asp Ile Asp Glu Leu Asp Ala Asp Ala Leu Ile Arg Leu Ala Thr
 1540 1545 1550

Gly Thr Ala Gly Pro Ala Asp Gly Thr Pro Ala Asp Gly Gly Pro Asp
 1555 1560 1565

15

Ala Ala Ala Thr Ala Pro Asp Gly Ala Pro Glu Gln
 1570 1575 1580

(2) INFORMATION FOR SEQ ID NO:12:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1891 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ser Pro Ser Met Asp Glu Val Leu Gly Ala Leu Arg Thr Ser Val
 1 5 10 15

30

Lys Glu Thr Glu Arg Leu Arg Arg His Asn Arg Glu Leu Leu Ala Gly
 20 25 30

35

Ala His Glu Pro Val Ala Ile Val Gly Met Ala Cys Arg Tyr Pro Gly
 35 40 45

Gly Val Ser Thr Pro Asp Asp Leu Trp Glu Leu Ala Ala Asp Gly Val
 50 55 60

40

Asp Ala Ile Thr Pro Phe Pro Ala Asp Arg Gly Trp Asp Glu Asp Ala
 65 70 75 80

Val Tyr Ser Pro Asp Pro Asp Thr Pro Gly Thr Thr Tyr Cys Arg Glu
 85 90 95

45

Gly Gly Phe Leu Thr Gly Ala Gly Asp Phe Asp Ala Ala Phe Phe Gly
 100 105 110

50

Ile Ser Pro Asn Glu Ala Leu Val Met Asp Pro Gln Gln Arg Leu Leu
 115 120 125

Leu Glu Thr Ser Trp Glu Thr Leu Glu Arg Ala Gly Ile Val Pro Ala
 130 135 140

55

Ser Leu Arg Gly Ser Arg Thr Gly Val Phe Val Gly Ala Ala His Thr
 145 150 155 160

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Gly Tyr Val Thr Asp Thr Ala Arg Ala Pro Glu Gly Thr Glu Gly Tyr
 165 170 175
 Leu Leu Thr Gly Asn Ala Asp Ala Val Met Ser Gly Arg Ile Ala Tyr
 5 180 185 190
 Ser Leu Gly Leu Glu Gly Pro Ala Leu Thr Ile Gly Thr Ala Cys Ser
 195 200 205
 Ser Ser Leu Val Ala Leu His Leu Ala Val Gln Ser Leu Arg Arg Gly
 10 210 215 220
 Glu Cys Asp Leu Ala Leu Ala Gly Gly Val Ala Val Met Pro Asp Pro
 225 230 235 240
 Thr Val Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Val Asp Gly
 15 245 250 255
 Arg Cys Lys Ala Phe Ala Glu Gly Ala Asp Gly Thr Ala Trp Ala Glu
 260 265 270
 Gly Val Gly Val Leu Leu Val Glu Arg Leu Ser Asp Ala Arg Arg Asn
 20 275 280 285
 Gly His Arg Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln Asp
 290 295 300
 Gly Ala Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ala Gln Gln Arg
 25 305 310 315 320
 Val Ile Arg Glu Ala Leu Ala Asp Ala Gly Leu Thr Pro Ala Asp Val
 325 330 335
 30 Asp Val Val Glu Ala His Gly Thr Gly Thr Ala Leu Gly Asp Pro Ile
 340 345 350
 Glu Ala Gly Ala Leu Leu Ala Thr Tyr Gly Arg Glu Arg Val Gly Asp
 35 355 360 365
 Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln Ala
 370 375 380
 Ala Ala Gly Val Gly Val Ile Lys Val Val Gln Ala Met Arg His
 40 385 390 395 400
 Gly Ser Leu Pro Arg Thr Leu His Val Asp Ala Pro Ser Ser Lys Val
 405 410 415
 Glu Trp Ala Ser Gly Ala Val Glu Leu Leu Thr Glu Gly Arg Ser Trp
 45 420 425 430
 Pro Arg Arg Val Glu Arg Val Arg Arg Ala Ala Val Ser Ala Phe Gly
 435 440 445
 Val Ser Gly Thr Asn Ala His Val Val Leu Glu Ala Pro Val Glu
 50 450 455 460
 Ala Gly Ser Glu His Gly Asp Gly Pro Gly Pro Asp Arg Pro Asp Ala
 465 470 475 480
 55 Val Thr Gly Pro Leu Pro Trp Val Leu Ser Ala Arg Ser Arg Glu Ala

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	485	490	495
	Leu Arg Gly Gln Ala Gly Arg Leu Ala Ala Leu Ala Arg Gln Gly Arg		
5	500	505	510
	Thr Glu Gly Thr Gly Gly Ser Gly Leu Val Val Pro Ala Ala Asp		
	515	520	525
10	Ile Gly Tyr Ser Leu Ala Thr Thr Arg Glu Thr Leu Glu His Arg Ala		
	530	535	540
	Val Ala Leu Val Gln Glu Asn Arg Thr Ala Gly Glu Asp Leu Ala Ala		
	545	550	555
15	Leu Ala Ala Gly Arg Thr Pro Glu Ser Val Val Thr Gly Val Ala Arg		
	565	570	575
	Arg Gly Arg Gly Ile Ala Phe Leu Cys Ser Gly Gln Gly Ala Gln Arg		
	580	585	590
20	Leu Gly Ala Gly Arg Glu Leu Arg Gly Arg Phe Pro Val Phe Ala Asp		
	595	600	605
	Ala Leu Asp Glu Ile Ala Ala Glu Phe Asp Ala His Leu Glu Arg Pro		
	610	615	620
25	Leu Leu Ser Val Met Phe Ala Glu Pro Ala Thr Pro Asp Ala Ala Leu		
	625	630	635
	640		
	Leu Asp Arg Thr Asp Tyr Thr Gln Pro Ala Leu Phe Ala Val Glu Thr		
	645	650	655
30	Ala Leu Phe Arg Leu Leu Glu Ser Trp Gly Leu Val Pro Asp Val Leu		
	660	665	670
	Val Gly His Ser Ile Gly Gly Leu Val Ala Ala His Val Ala Gly Val		
	675	680	685
35	Phe Ser Ala Ala Asp Ala Ala Arg Leu Val Ser Ala Arg Gly Arg Leu		
	690	695	700
	Met Arg Ala Leu Pro Glu Gly Gly Ala Met Ala Ala Val Gln Ala Thr		
	705	710	715
40	720		
	Glu Arg Glu Ala Ala Leu Glu Pro Val Ala Ala Gly Gly Ala Val		
	725	730	735
	Val Ala Ala Val Asn Gly Pro Gln Ala Leu Val Leu Ser Gly Asp Glu		
	740	745	750
45	Ala Ala Val Leu Ala Ala Gly Glu Leu Ala Ala Arg Gly Arg Arg		
	755	760	765
	Thr Lys Arg Leu Arg Val Ser His Ala Phe His Ser Pro Arg Met Asp		
50	770	775	780
	Ala Met Leu Ala Asp Phe Arg Ala Val Ala Asp Thr Val Asp Tyr His		
	785	790	795
	800		
55	Ala Pro Arg Leu Pro Val Val Ser Glu Val Thr Gly Asp Leu Ala Asp		
	805	810	815

Ala Ala Gln Leu Thr Asp Pro Gly Tyr Trp Thr Arg Gln Val Arg Gln
 820 825 830

5 Pro Val Arg Phe Ala Asp Ala Val Arg Thr Ala Ser Ala Arg Asp Ala
 835 840 845

Ala Thr Phe Ile Glu Leu Gly Pro Asp Ala Val Leu Cys Gly Met Ala
 850 855 860

10 Glu Glu Ser Leu Ala Ala Glu Ala Asp Val Val Phe Ala Pro Ala Leu
 865 870 875 880

Arg Arg Gly Arg Pro Glu Gly Asp Thr Val Leu Arg Ala Ala Ser
 885 890 895

15 Ala Tyr Val Arg Gly Ala Gly Leu Asp Trp Ala Ala Leu Tyr Gly Gly
 900 905 910

Thr Gly Ala Arg Arg Thr Asp Leu Pro Thr Tyr Ala Phe Gln His Ser
 20 915 920 925

Arg Tyr Trp Leu Ala Pro Ala Ser Ala Ala Val Ala Pro Ala Thr Ala
 930 935 940

25 Ala Pro Ser Val Arg Ser Val Pro Glu Ala Glu Gln Asp Gly Ala Leu
 945 950 955 960

Trp Ala Ala Val His Ala Gly Asp Val Ala Ser Ala Ala Arg Leu
 965 970 975

Gly Ala Asp Asp Ala Gly Ile Glu His Glu Leu Arg Ala Val Leu Pro
 30 980 985 990

His Leu Ala Ala Trp His Asp Arg Asp Arg Ala Thr Ala Arg Thr Ala
 995 1000 1005

35 Gly Leu His Tyr Arg Val Thr Trp Gln Ala Ile Glu Ala Asp Ala Val
 1010 1015 1020

Arg Phe Ser Pro Ser Asp Arg Trp Leu Met Val Glu His Gly Gln His
 1025 1030 1035 1040

40 Thr Glu Cys Ala Asp Ala Ala Glu Arg Ala Leu Arg Ala Ala Gly Ala
 1045 1050 1055

Glu Val Thr Arg Leu Val Trp Pro Leu Glu Gln His Thr Gly Ser Pro
 1060 1065 1070

45 Arg Thr Glu Thr Pro Asp Arg Gly Thr Leu Ala Ala Arg Leu Ala Glu
 1075 1080 1085

Leu Ala Arg Ser Pro Glu Gly Leu Ala Gly Val Leu Leu Leu Pro Asp
 50 1090 1095 1100

Ser Gly Gly Ala Ala Val Ala Gly His Pro Gly Leu Asp Gln Gly Thr
 1105 1110 1115 1120

Ala Ala Val Leu Leu Thr Ile Gln Ala Leu Thr Asp Ala Ala Val Arg
 55 1125 1130 1135

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Ala Pro Leu Trp Val Val Thr Arg Gly Ala Val Ala Val Gly Ser Gly
 1140 1145 1150
 5 Glu Val Pro Cys Ala Val Gly Ala Arg Val Trp Gly Leu Gly Arg Val
 1155 1160 1165
 Ala Ala Leu Glu Val Pro Val Gln Trp Gly Gly Leu Val Asp Val Ala
 1170 1175 1180
 10 Val Gly Ala Gly Val Arg Glu Trp Arg Arg Val Val Gly Val Val Ala
 1185 1190 1195 1200
 Gly Gly Gly Glu Asp Gln Val Ala Val Arg Gly Gly Val Phe Gly
 1205 1210 1215
 15 Arg Arg Leu Val Gly Val Gly Val Arg Gly Ser Gly Val Trp Arg
 1220 1225 1230
 Ala Arg Gly Cys Val Val Val Thr Gly Gly Leu Gly Gly Val Gly Gly
 1235 1240 1245
 20 His Val Ala Arg Trp Leu Ala Arg Ser Gly Ala Glu His Val Val Leu
 1250 1255 1260
 Ala Gly Arg Arg Gly Gly Val Val Gly Ala Val Glu Leu Glu Arg
 25 1265 1270 1275 1280
 Glu Leu Val Gly Leu Gly Ala Lys Val Thr Phe Val Ser Cys Asp Val
 1285 1290 1295
 30 Gly Asp Arg Ala Ser Val Val Gly Leu Leu Gly Val Val Glu Gly Leu
 1300 1305 1310
 Gly Val Pro Leu Arg Gly Val Phe His Ala Ala Gly Val Ala Gln Val
 35 1315 1320 1325
 Ser Gly Leu Gly Glu Val Ser Leu Ala Glu Ala Gly Gly Val Leu Gly
 1330 1335 1340
 Gly Lys Ala Val Gly Ala Glu Leu Leu Asp Glu Leu Thr Ala Gly Val
 40 1345 1350 1355 1360
 Glu Leu Asp Ala Phe Val Leu Phe Ser Ser Gly Ala Gly Val Trp Gly
 1365 1370 1375
 Ser Gly Gly Gln Ser Val Tyr Ala Ala Ala Asn Ala His Leu Asp Ala
 45 1380 1385 1390
 Leu Ala Glu Arg Arg Ala Gln Gly Arg Pro Ala Thr Ser Val Ala
 1395 1400 1405
 Trp Gly Pro Trp Asp Gly Asp Gly Met Gly Glu Met Ala Pro Glu Gly
 50 1410 1415 1420
 Tyr Phe Ala Arg His Gly Val Ala Pro Leu His Pro Glu Thr Ala Leu
 1425 1430 1435 1440
 Thr Ala Leu His Gln Ala Ile Asp Gly Gly Glu Ala Thr Val Thr Val
 55 1445 1450 1455
 Ala Asp Ile Asp Trp Glu Arg Phe Ala Pro Gly Phe Thr Ala Phe Arg

	1460	1465	1470
	Pro Ser Pro Leu Ile Ala Gly Ile Pro Ala Ala Arg Thr Ala Pro Ala		
5	1475	1480	1485
	Ala Gly Arg Pro Ala Glu Asp Thr Pro Thr Ala Pro Gly Leu Leu Arg		
	1490	1495	1500
10	Ala Arg Pro Glu Asp Arg Pro Arg Leu Ala Leu Asp Leu Val Leu Arg		
	1505	1510	1515
	His Val Ala Ala Val Leu Gly His Ser Glu Asp Ala Arg Val Asp Ala		
	1525	1530	1535
15	Arg Ala Pro Phe Arg Asp Leu Gly Phe Asp Ser Leu Ala Ala Val Arg		
	1540	1545	1550
	Leu Arg Arg Arg Leu Ala Glu Asp Thr Gly Leu Asp Leu Pro Gly Thr		
	1555	1560	1565
20	Leu Val Phe Asp His Glu Asp Pro Thr Ala Leu Ala His His Leu Ala		
	1570	1575	1580
	Gly Leu Ala Asp Ala Gly Thr Pro Gly Pro Gln Glu Gly Thr Ala Arg		
	1585	1590	1595
	Ala Glu Ser Gly Leu Phe Ala Ser Phe Arg Ala Ala Val Glu Gln Arg		
25	1605	1610	1615
	Arg Ser Ser Glu Val Val Glu Leu Met Ala Asp Leu Ala Ala Phe Arg		
	1620	1625	1630
30	Pro Ala Tyr Ser Arg Gln His Pro Gly Ser Gly Arg Pro Ala Pro Val		
	1635	1640	1645
	Pro Leu Ala Thr Gly Pro Ala Thr Arg Pro Thr Leu Tyr Cys Cys Ala		
35	1650	1655	1660
	Gly Thr Ala Val Gly Ser Gly Pro Ala Glu Tyr Val Pro Phe Ala Glu		
	1665	1670	1675
	Gly Leu Arg Gly Val Arg Glu Thr Val Ala Leu Pro Leu Ser Gly Phe		
	1685	1690	1695
40	Gly Asp Pro Ala Glu Pro Met Pro Ala Ser Leu Asp Ala Leu Ile Glu		
	1700	1705	1710
	Val Gln Ala Asp Val Leu Leu Glu His Thr Ala Gly Lys Pro Phe Ala		
45	1715	1720	1725
	Leu Ala Gly His Ser Ala Gly Ala Asn Ile Ala His Ala Leu Ala Ala		
	1730	1735	1740
50	Arg Leu Glu Glu Arg Gly Ser Gly Pro Ala Ala Val Val Leu Met Asp		
	1745	1750	1755
	Val Tyr Arg Pro Glu Asp Pro Gly Ala Met Gly Glu Trp Arg Asp Asp		
	1765	1770	1775
55	Leu Leu Ser Trp Ala Leu Glu Arg Ser Thr Val Pro Leu Glu Asp His		
	1780	1785	1790

Arg Leu Thr Ala Met Ala Gly Tyr Gln Arg Leu Val Leu Gly Thr Arg
 1795 1800 1805
 5 Leu Thr Ala Leu Glu Ala Pro Val Leu Leu Ala Arg Ala Ser Glu Pro
 1810 1815 1820
 Leu Cys Ala Trp Pro Pro Ala Gly Gly Ala Arg Gly Asp Trp Arg Ser
 1825 1830 1835 1840
 10 Gln Val Pro Phe Ala Arg Thr Val Ala Asp Val Pro Gly Asn His Phe
 1845 1850 1855
 Thr Met Leu Thr Glu His Ala Arg His Thr Ala Ser Leu Val His Glu
 1860 1865 1870
 15 Trp Leu Asp Ser Leu Pro His Gln Pro Gly Pro Ala Pro Leu Thr Gly
 1875 1880 1885
 Gly Lys His
 20 1890

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13987 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 350..13987

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACCGCTCGG GGAGACCTGA CATATTCGTC GCGAAGTGGT TGTCCGCCGC GCGAGGTACT	60
GAAATCTTCT CCGCTCGCCC AGGACTCCGC GTGCAGGTCA CCGGAGTGCG CGACCGGCCG	120
GGACGTCGGA GCGCCGACCC TGCGGACCTG GTGCGATGCC GTGTGGTCCC GCATGATCCC	180
GCGCCGTCTC CGGTGACGAG AATCGGTGGA CAATCTCCGA ACTTGACACCA ATTGATTGTC	240
45 GTTCACCGGC CGTTCCCTGTC GCCCGGCAGT TCGCCCGCTG TACGCTCGGG AAGATCAAGA	300
AAAGGCAGAA AAGCCACGGC GTGGTACGGC GAACATATGA GGGATGCAG GTG TCT Met Ser 1	355
50 GGA GAA CTC GCG ATT TCC CGC AGT GAC GAC CGG TCC GAC GCC GTT GCC Gly Glu Leu Ala Ile Ser Arg Ser Asp Asp Arg Ser Asp Ala Val Ala 5 10 15	403
55 GTG GTC GGA ATG GCG TGC CGG TTT CCC GGC GCC CCG GGA ATT GCC GAA Val Val Gly Met Ala Cys Arg Phe Pro Gly Ala Pro Gly Ile Ala Glu	451

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	20	25	30	
5	TTC TGG GAA CTG CTG CGC AGC GGA CGC GGT ATG CCC ACC CGT CAG GAC Phe Trp Glu Leu Leu Arg Ser Gly Arg Gly Met Pro Thr Arg Gln Asp 35 40 45 50			499
	GAC GGC ACC TGG CGG GCC CTG GAG GAC CAC GCC GGC TTC GAC GCC Asp Gly Thr Trp Arg Ala Ala Leu Glu Asp His Ala Gly Phe Asp Ala 55 60 65			547
10	GGG TTC TTC GGC ATG AAC GCC CGG CAG GCC GCC ACC GAC CCG CAG Gly Phe Phe Gly Met Asn Ala Arg Gln Ala Ala Ala Thr Asp Pro Gln 70 75 80			595
15	CAC CGA CTG ATG CTG GAA CTC GGA TGG GAG GCA CTG GAG GAC GCG GGC His Arg Leu Met Leu Glu Leu Gly Trp Glu Ala Leu Glu Asp Ala Gly 85 90 95			643
20	ATC GTC CCC GGC GAT CTC ACC GGC ACC GAC ACC GGA GTC TTC GCC GGC Ile Val Pro Gly Asp Leu Thr Gly Thr Asp Thr Gly Val Phe Ala Gly 100 105 110			691
	GTG GCG TCC GAC GAC TAT GCC GTT CTC ACC CGC CGT TCC GCC GTC TCC Val Ala Ser Asp Asp Tyr Ala Val Leu Thr Arg Arg Ser Ala Val Ser 115 120 125 130			739
25	GCC GGG GGA TAC ACC GCC ACG GGG CTG CAC CGC GCC CTG GCC GCC AAC Ala Gly Gly Tyr Thr Ala Thr Gly Leu His Arg Ala Leu Ala Ala Asn 135 140 145			787
30	CGC CTC TCC CAC TTC CTG GGC CTG CGC GGC CCC AGC CTG GTC GTC GAC Arg Leu Ser His Phe Leu Gly Leu Arg Gly Pro Ser Leu Val Val Asp 150 155 160			835
	TCG GCC CAG TCC GCC TCA CTG GTG GCC GTC CAG CTC GCC TGC GAG AGT Ser Ala Gln Ser Ala Ser Leu Val Ala Val Gln Leu Ala Cys Glu Ser 165 170 175			883
35	CTG CGC CGG GGT GAG ACG TCG CTC GCC GTC GCG GGC GGT GTC AAC CTC Leu Arg Arg Gly Glu Thr Ser Leu Ala Val Ala Gly Gly Val Asn Leu 180 185 190			931
40	ATC CTC ACC GAG GAG AGC ACC ACC GTC ATG GAG CGT ATG GGA GCG CTC Ile Leu Thr Glu Glu Ser Thr Thr Val Met Glu Arg Met Gly Ala Leu 195 200 205 210			979
45	TCA CCC GAC GGC CGC TGC CAC ACC TTC GAC GCC CGC GCC AAC GGC TAC Ser Pro Asp Gly Arg Cys His Thr Phe Asp Ala Arg Ala Asn Gly Tyr 215 220 225			1027
	GTA CGC GGC GAG GGC GGC GGA GCC GTC GTG CTC AAG CCA CTG GAC GCC Val Arg Gly Glu Gly Gly Ala Val Val Leu Lys Pro Leu Asp Ala 230 235 240			1075
50	GCA CTC GCC GAC GGC GAC CGC GTG TAC TGC GTC ATC AAG GGA GGT GCC Ala Leu Ala Asp Gly Asp Arg Val Tyr Cys Val Ile Lys Gly Gly Ala 245 250 255			1123
55	GTC AAC AAC GAC GGC GGC GCG AGC CTC ACC ACT CCC GAC CGG GAG Val Asn Asn Asp Gly Gly Ala Ser Leu Thr Thr Pro Asp Arg Glu			1171

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	260	265	270	
5	GCG CAG GAA GCT GTG CTG CGC CAG GCC TAC CGG CGG GCG GGC GTC AGC Ala Gln Glu Ala Val Leu Arg Gln Ala Tyr Arg Arg Ala Gly Val Ser 275 280 285 290			1219
	ACC GGC GCC GTC CGC TAC GTC GAG CTG CAC GGG ACC GGC ACC CGG GCC Thr Gly Ala Val Arg Tyr Val Glu Leu His Gly Thr Gly Thr Arg Ala 295 300 305			1267
10	GGC GAC CCC GTC GAG GCG GCC GCA CTG GGC GCC GTG CTC GGG GCG GGG Gly Asp Pro Val Glu Ala Ala Ala Leu Gly Ala Val Leu Gly Ala Gly 310 315 320			1315
15	GCG GAC AGC GGC CGC AGC ACG CCG CTC GCC GTC GGC TCG GTG AAG ACC Ala Asp Ser Gly Arg Ser Thr Pro Leu Ala Val Gly Ser Val Lys Thr 325 330 335			1363
20	AAC GTC GGC CAT CTG GAG GGC GCG GCG ATC GTC GGA CTG ATC AAG Asn Val Gly His Leu Glu Gly Ala Ala Gly Ile Val Gly Leu Ile Lys 340 345 350			1411
	GCC ACG CTG TGC GTA CGG AAG GGC GAA CTC GTC CCC AGC CTC AAC TTC Ala Thr Leu Cys Val Arg Lys Gly Glu Leu Val Pro Ser Leu Asn Phe 355 360 365 370			1459
25	AGC ACG CCG AAC CCT GAC ATC CCC CTC GAC GAC CTG CCG CTG CCC GTC Ser Thr Pro Asn Pro Asp Ile Pro Leu Asp Asp Leu Arg Leu Arg Val 375 380 385			1507
30	CAG ACC GAA CGG CAG GAG TGG AAC GAG GAG GAC GAC CGG CCG CCG GTG Gln Thr Glu Arg Gln Glu Trp Asn Glu Asp Asp Arg Pro Arg Val 390 395 400			1555
	GCC GGC GTC TCC TCC TTC GGT ATG GGC GGA ACC AAT GTC CAC CTC GTG Ala Gly Val Ser Ser Phe Gly Met Gly Gly Thr Asn Val His Leu Val 405 410 415			1603
35	ATC GCG GAG GCT CCG GCC GCG GGG TCC TCC GGG GCG GGG GGT TCG Ile Ala Glu Ala Pro Ala Ala Gly Ser Ser Gly Ala Gly Gly Ser 420 425 430			1651
40	GCG GCT GGT TCC GGT GCC GGT ATC AGC GCT GTT TCT GGT GTG GTG CCG Gly Ala Gly Ser Gly Ala Gly Ile Ser Ala Val Ser Gly Val Val Pro 435 440 445 450			1699
	GTG GTG GTT TCG GGG CGT TCG CGG GTG GTG GTG CGG GAG GCT GCG GGC Val Val Val Ser Gly Arg Ser Arg Val Val Val Arg Glu Ala Ala Gly 455 460 465			1747
45	CGG TTG GCG GAG GTG GTG GAG GCC GGT GGT GTG GGG CTG GCG GAT GTG Arg Leu Ala Glu Val Val Glu Ala Gly Gly Val Gly Leu Ala Asp Val 470 475 480			1795
50	GCG GTG ACG ATG GCG GAC CGG TCG CGG TTT GGG TAT CGG GCG GTT GTG Ala Val Thr Met Ala Asp Arg Ser Arg Phe Gly Tyr Arg Ala Val Val 485 490 495			1843
55	CTG GCT CGG GGT GAG GCT GAG CTT GCC GGG CGT TTG CGG GCG TTG GCG Leu Ala Arg Gly Glu Ala Glu Leu Ala Gly Arg Leu Arg Ala Leu Ala			1891

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	500	505	510	
5	GGG GGT GAT CCG GAC GCG GGT GTG GTC ACC GGT GCG GTT CTC GAC GGT Gly Gly Asp Pro Asp Ala Gly Val Val Thr Gly Ala Val Leu Asp Gly 515 520 525 530			1939
	GGT GTG GTT GTC GGT GCT GCC CCC GGC GGT GCC GGT GCT GCC GGT GGT Gly Val Val Val Gly Ala Ala Pro Gly Gly Ala Gly Ala Ala Gly Gly 535 540 545			1987
10	GCC GGT GCT GCC GGT GCT GCC GGT GGT GGG GGC GTG GTG TTG GTT TTC Ala Gly Ala Ala Gly Gly Ala Gly Gly Gly Val Val Leu Val Phe 550 555 560			2035
15	CCT GGT CAG GGG ACG CAG TGG GTG GGG ATG CCG GGT GCG GGG CTG CTC CGG Pro Gly Gln Gly Thr Gln Trp Val Gly Met Gly Ala Gly Leu Leu Gly 565 570 575			2083
	TCT TCG GAG GTG TTT GCG GCG TCG ATG CCG GAG TGT GCG CGG CCC CTG Ser Ser Glu Val Phe Ala Ala Ser Met Arg Glu Cys Ala Arg Ala Leu 580 585 590			2131
20	AGT GTT CAT GTG GGG TGG GAT TTG CTG GAG GTG GTG TCG CCC CGG GCC Ser Val His Val Gly Trp Asp Leu Leu Glu Val Val Ser Gly Gly Ala 595 600 605 610			2179
25	GGG TTG GAG CGG GTG GAT GTG GTG CAG CCG GTG ACG TGG GCG GTG ATG Gly Leu Glu Arg Val Asp Val Val Gln Pro Val Thr Trp Ala Val Met 615 620 625			2227
30	GTG TCG CTG GCC CGG TAC TGG CAG GCG ATG GGT GTG GAC GTG GCT CGC Val Ser Leu Ala Arg Tyr Trp Gln Ala Met Gly Val Asp Val Ala Ala 630 635 640			2275
	GTG GTG GGT CAT TCC CAG GGG GAG ATC GCC GCT GCC ACG GTG GCG GGG Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala Thr Val Ala Gly 645 650 655			2323
35	GCG TTG TCG CTG GAG GAT GCG GCG GCT GTG GTC GCT CTG CGG GCG GGG Ala Leu Ser Leu Glu Asp Ala Ala Ala Val Val Ala Leu Arg Ala Gly 660 665 670			2371
40	TTG ATT GGC CGG TAT CTG GCG GGT CGT GGT GCG ATG GCG GCT GTT CCG Leu Ile Gly Arg Tyr Leu Ala Gly Arg Gly Ala Met Ala Ala Val Pro 675 680 685 690			2419
45	CTG CCT GCC GGC GAG GTC GAG GCC GGG CTG GCG AAG TGG CCG GGT GTG Leu Pro Ala Gly Glu Val Glu Ala Gly Leu Ala Lys Trp Pro Gly Val 695 700 705			2467
	GAG GTC GCG GCG GTC AAC GGT CCG GCG TCT ACG GTG GTT TCC GGG GAT Glu Val Ala Ala Val Asn Gly Pro Ala Ser Thr Val Val Ser Gly Asp 710 715 720			2515
50	CGG CGG GCG GTG GCC GGT TAT GTG GCC GTC TGT CAG GCG GAG GGT GTG Arg Arg Ala Val Ala Gly Tyr Val Ala Val Cys Gln Ala Glu Gly Val 725 730 735			2563
55	CAG GCC CGG TTG ATA CCG GTG GAC TAC GCC TCT CAC TCC CGC CAT GTG Gln Ala Arg Leu Ile Pro Val Asp Tyr Ala Ser His Ser Arg His Val			2611

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	740	745	750	
5	GAG GAC CTG AAG GGC GAG TTG GAG CGG GTG CTG TCC GGT ATC CGC CCC Glu Asp Leu Lys Gly Glu Leu Glu Arg Val Leu Ser Gly Ile Arg Pro 755 760 765 770			2659
	CGC AGT CCG CGG GTG CCG GTG TGT TCC ACC GTC GCC GGA GAG CAG CCG Arg Ser Pro Arg Val Pro Val Cys Ser Thr Val Ala Gly Glu Gln Pro 775 780 785			2707
10	GGC GAG CCG GTT TTC GAT GCG GGG TAT TGG TTC CGT AAT CTG CGG AAC Gly Glu Pro Val Phe Asp Ala Gly Tyr Trp Phe Arg Asn Leu Arg Asn 790 795 800			2755
~ 15	CGG GTT GAG TTC TCC GCG GTG GTC GGT GGT TTG TTG GAG GAG GGC CAC Arg Val Glu Phe Ser Ala Val Gly Gly Leu Leu Glu Gly His 805 810 815			2803
20	CGT CGG TTC ATC GAG GTC AGT GGC CAC CCG GTA CTC GTC CAT GCG ATC Arg Arg Phe Ile Glu Val Ser Ala His Pro Val Leu Val His Ala Ile 820 825 830			2851
	GAG CAG ACG GCC GAG GCC GCG GAC CGG AGT GTC CAT GCC ACC GGG ACC Glu Gln Thr Ala Glu Ala Asp Arg Ser Val His Ala Thr Gly Thr 835 840 845 850			2899
25	CTG CGC CGC CAG GAC GAC ACC CCG CAC CGC CTG CTG ACC TCC ACC GCC Leu Arg Arg Gln Asp Asp Ser Pro His Arg Leu Leu Thr Ser Thr Ala 855 860 865			2947
30	GAG GCC TGG GCC CAC GGC GCC ACC CTC ACC TGG GAC CCC GCC CTG CCC Glu Ala Trp Ala His Gly Ala Thr Leu Thr Trp Asp Pro Ala Leu Pro 870 875 880			2995
	CCA GGC CAC CTC ACC ACC CTC CCC ACC TAC CCC TTC AAC CAC CAC CAC Pro Gly His Leu Thr Thr Leu Pro Thr Tyr Pro Phe Asn His His His 885 890 895			3043
35	TAC TGG CTC GAC ACC ATT GAC GGG GGC GGA GGG GAC GAC GCG ACC CAG Tyr Trp Leu Asp Thr Ile Asp Gly Gly Gly Asp Asp Ala Thr Gln 900 905 910			3091
40	GAG AAG GAG AGC GGC CCT CTG ACG CGG GAA CTG CGT GGG CTG CCG TCC Glu Lys Glu Ser Gly Pro Leu Thr Arg Glu Leu Arg Gly Leu Pro Ser 915 920 925 930			3139
45	TCT CAG AAG CAA CTG GGT TTC CTG CTC GAT CTG GTG TGC CGG CAC ACG Ser Gln Lys Gln Leu Gly Phe Leu Leu Asp Leu Val Cys Arg His Thr 935 940 945			3187
	GCC GTC GTA CTC GGC CTG GAC ACG GCC GCG GAG GTG GAC CCG GAC CTG Ala Val Val Leu Gly Leu Asp Thr Ala Ala Glu Val Asp Pro Asp Leu 950 955 960			3235
50	TCC TTC AAG AAG CAG GGC ATC CAG TCC ATG ACC GGC GTC GAG CTG CGC Ser Phe Lys Lys Gln Gly Ile Gln Ser Met Thr Gly Val Glu Leu Arg 965 970 975			3283
55	AAC AGG CTG CTG ACC GAG ACC GGC CTG GCA TTG CCC ACC ACC CTC GTC Asn Arg Leu Leu Thr Glu Thr Gly Leu Ala Leu Pro Thr Thr Leu Val			3331

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	980	985	990	
5	TAC GAC CGG CCC ACC CCT CGC GCC CTG GCG CAG TTC CTC CAC ACC GAG Tyr Asp Arg Pro Thr Pro Arg Ala Leu Ala Gln Phe Leu His Thr Glu 995 1000 1005 1010			3379
	TTG CTC GAC GGC TCC CCC TCG GGC TCC GTC CTC GCA CCG GCG CAG AAG Leu Leu Asp Gly Ser Pro Ser Gly Ser Val Leu Ala Pro Ala Gln Lys 1015 1020 1025			3427
10	AGC TTC GAG GCC GGC GGG CCC GGA GTG CTC TCG TCG GCC GCG GTA GGG Ser Phe Glu Ala Gly Gly Pro Gly Val Leu Ser Ser Ala Ala Val Gly 1030 1035 1040			3475
15	GTG TCG GAC GCC CGG GGC AGC CGG GAC GAC GAC CCG ATC GCC Val Ser Asp Ala Arg Gly Gly Ser Arg Asp Asp Asp Pro Ile Ala 1045 1050 1055			3523
	ATC GTG GGT GTC GGC TGC CGG CTC CCC GGC GTC GAC TCG CGC GCC Ile Val Gly Val Gly Cys Arg Leu Pro Gly Gly Val Asp Ser Arg Ala			3571
20	1060 1065 1070			
	GCT CTC TGG GAG CTG CTG GAG TCC GGC GCC GAC GCC ATC TCG TCC TTC Ala Leu Trp Glu Leu Leu Glu Ser Gly Ala Asp Ala Ile Ser Ser Phe 1075 1080 1085 1090			3619
25	CCC ACC GAC CGC GGC TGG GAC CTC GAC GGG CTG TAC GAC CCC GAG CCC Pro Thr Asp Arg Gly Trp Asp Leu Asp Gly Leu Tyr Asp Pro Glu Pro 1095 1100 1105			3667
	GGG ACG CCC GGC AAG ACC TAT GTG CGG GAG GGC GGG TTC CTG CAC TCG Gly Thr Pro Gly Lys Thr Tyr Val Arg Glu Gly Gly Phe Leu His Ser 30 1110 1115 1120			3715
	GCG GCC GAG TTC GAC GCG GAG TTC TTC GGG ATA TCG CCG CGC GAG GCC Ala Ala Glu Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg Glu Ala 1125 1130 1135			3763
35	ACG GCC ATG GAC CCG CAG CGC TTG CTG CTG GAA GCG TCG TGG GAG Thr Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Ala Ser Trp Glu 1140 1145 1150			3811
40	GCC CTC GAG GAC GCC GGA GTG CTC CCC GAG TCA CTG CGC GGC GGC GAC Ala Leu Glu Asp Ala Gly Val Leu Pro Glu Ser Leu Arg Gly Gly Asp 1155 1160 1165 1170			3859
	GCC GGA GTG TTC GTC GGC GCC ACC GCA CCG GAG TAC GGG CCG AGG CTT Ala Gly Val Phe Val Gly Ala Thr Ala Pro Glu Tyr Gly Pro Arg Leu 45 1175 1180 1185			3907
	CAC GAG GGA GCG GAC GGA TAC GAG GGG TAC CTG CTC ACC GGC ACC ACC His Glu Gly Ala Asp Gly Tyr Glu Gly Tyr Leu Leu Thr Gly Thr Thr 1190 1195 1200			3955
50	GCG AGC GTG GCC TCC GGC CGG ATC GCC TAC ACC CTC GGC ACC GGC GGA Ala Ser Val Ala Ser Gly Arg Ile Ala Tyr Thr Leu Gly Thr Gly Gly 1205 1210 1215			4003
55	CCG GCG CTC ACC GTC GAC ACC GCG TGC TCC TCG TCC CTG GTG GCG CTG Pro Ala Leu Thr Val Asp Thr Ala Cys Ser Ser Leu Val Ala Leu			4051

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	1220	1225	1230	
5	CAC CTG GCC GTG CAG GCG CTG CGC CGG GGC GAG TGC GGG CTG GCT CTG His Leu Ala Val Gln Ala Leu Arg Arg Gly Glu Cys Gly Leu Ala Leu 1235 1240 1245 1250			4099
	GCG GGC GGC GCC ACG GTG ATG TCG GGG CCC GGC ATG TTC GTG GAG TTC Ala Gly Gly Ala Thr Val Met Ser Gly Pro Gly Met Phe Val Glu Phe 1255 1260 1265			4147
10	TCG CGG CAG CGC GGG CTC GCC CCC GAC GGC CGC TGC ATG CCG TTC TCC Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg Cys Met Pro Phe Ser 1270 1275 1280			4195
15	GCC GAT GCC GAC GGT ACG GCC TGG TCC GAG GGT GTC GCC GTA CTC GCA Ala Asp Ala Asp Gly Thr Ala Trp Ser Glu Gly Val Ala Val Leu Ala 1285 1290 1295			4243
20	CTG GAG CGG CTC TCC GAC GCC CGG CGT GCG GGA CAC CGG GTG CTG CGC Leu Glu Arg Leu Ser Asp Ala Arg Arg Ala Gly His Arg Val Leu Gly 1300 1305 1310			4291
	GTG GTG CGG GGC AGT GCG GTC AAC CAG GAC GGT GCC AGC AAC GCC CTG Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu 1315 1320 1325 1330			4339
25	ACC GCT CCC AAC CGC TCC GCG CAG GAG GGC GTC ATC CGA GCT GCC CTG Thr Ala Pro Asn Arg Ser Ala Gln Glu Gly Val Ile Arg Ala Ala Leu 1335 1340 1345			4387
30	GCC GAC GCC GGC CTC GCG CCG GGT GAC GTG GAC GCG GTG GAG GCG CAC Ala Asp Ala Gly Leu Ala Pro Gly Asp Val Asp Ala Val Glu Ala His 1350 1355 1360			4435
	GGT ACG GGG ACG GCG CTG GGC GAT CCG ATC GAG GCG AGC GCG CTG CTG Gly Thr Gly Thr Ala Leu Gly Asp Pro Ile Glu Ala Ser Ala Leu Leu 1365 1370 1375			4483
35	GCC ACG TAC GGG CGT GAG CGG GTG GGC GAC CCC TTG TGG CTC GGG TCG Ala Thr Tyr Gly Arg Glu Arg Val Gly Asp Pro Leu Trp Leu Gly Ser 1380 1385 1390			4531
40	CTG AAG TCC AAC GTC GGT CAC ACC CAG GCC GCG GGG GCC GCG GGT Leu Lys Ser Asn Val Gly His Thr Gln Ala Ala Ala Gly Ala Ala Gly 1395 1400 1405 1410			4579
45	GTG GTC AAG ATG CTG CTT GCC CTG GAG CAC GGC ACG CTG CCG CGG ACA Val Val Lys Met Leu Leu Ala Leu Glu His Gly Thr Leu Pro Arg Thr 1415 1420 1425			4627
	CTT CAC GCG GAC CGG CCC AGC ACG CAC GTC GAC TGG TCG TCG GGC ACC Leu His Ala Asp Arg Pro Ser Thr His Val Asp Trp Ser Ser Gly Thr 1430 1435 1440			4675
50	GTC GCC CTG CTG GCA GAG GCG CGC CGG TGG CCC CGG CGG TCG GAC CGC Val Ala Leu Leu Ala Glu Ala Arg Arg Trp Pro Arg Arg Ser Asp Arg 1445 1450 1455			4723
55	CCG CGC CGG GCG GCT GTG TCG TCG TTC GGG ATC AGT GGG ACG AAC GCG Pro Arg Arg Ala Ala Val Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala			4771

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	1460	1465	1470	
5	CAT CTG ATC ATC GAG GAG GCG CCG GAG TGG GTC GAG GAC ATC GAC GGC His Leu Ile Ile Glu Ala Pro Glu Trp Val Glu Asp Ile Asp Gly 1475 1480 1485 1490			4819
	GTC GCT CCT GAC CGC GGT ACC GCG GAC GCG GCT GCT CCG TCG CCG Val Ala Ala Pro Asp Arg Gly Thr Ala Asp Ala Ala Pro Ser Pro 1495 1500 1505			4867
10	CTG TTG TTG TCC GCG CGG TCG GAG GGG GCG TTG CGG GCG CAG GCG GTG Leu Leu Leu Ser Ala Arg Ser Glu Gly Ala Leu Arg Ala Gln Ala Val 1510 1515 1520			4915
15	CGG TTG GGT GAG TAC GTG GAG CGG GTG GGT GCG GAT CCG CCG GAT GTG Arg Leu Gly Glu Tyr Val Glu Arg Val Gly Ala Asp Pro Arg Asp Val 1525 1530 1535			4963
20	GCT TAT TCG CTG GCT TCG ACC CGG ACT CTT TTC GAG CAC CGT GCG GTG Ala Tyr Ser Leu Ala Ser Thr Arg Thr Leu Phe Glu His Arg Ala Val 1540 1545 1550			5011
	GTG CCG TGT GGT GGG CGT GGG GAG CTC GTC GCT GCT CTT GGT GGG TTT Val Pro Cys Gly Gly Arg Gly Glu Leu Val Ala Ala Leu Gly Gly Phe 1555 1560 1565 1570			5059
25	GCT GCC GGG AGG GTG TCT CGG CGT CTG CGG TCC GGG CGG GCT GTG CCG Ala Ala Gly Arg Val Ser Gly Gly Val Arg Ser Gly Arg Ala Val Pro 1575 1580 1585			5107
30	GGT CGG GTG GGG GTG TTG TTC ACG GGT CAG GGT GCG CAG TGG GTT GGT Gly Gly Val Gly Val Leu Phe Thr Gly Gln Gly Ala Gln Trp Val Gly 1590 1595 1600			5155
35	ATG GGG CGT GGG TTG TAT GCG GGG GGT GGG GTG TTT GCG GAG GTG CTG Met Gly Arg Gly Leu Tyr Ala Gly Gly Val Phe Ala Glu Val Leu 1605 1610 1615			5203
	GAT GAG GTG TTG TCG ATG GTG GGG GAG GTG GAT GGT CGG TCG TTG CGG Asp Glu Val Leu Ser Met Val Gly Glu Val Asp Gly Arg Ser Leu Arg 1620 1625 1630			5251
40	GAT GTG ATG TTC GGC GAC GTC GAC GTG GAC GCG GGT GCC GGG GCT GAT Asp Val Met Phe Gly Asp Val Asp Val Asp Ala Gly Ala Gly Ala Asp 1635 1640 1645 1650			5299
45	GCG GGT GCC GGT GCG GGT GCT GGG GTC GGT TCT GGT TCC GGT TCT GTG Ala Gly Ala Gly Ala Gly Val Gly Ser Gly Ser Gly Ser Val 1655 1660 1665			5347
	GGT GGG TTG TTG GGT CGG ACG GAG TTT GCT CAG CCT GCG CTG TTT GCG Gly Gly Leu Leu Gly Arg Thr Glu Phe Ala Gln Pro Ala Leu Phe Ala 1670 1675 1680			5395
50	TTG GAG GTG GCG TTG TTC CGG GCG TTG GAG GCT CGG GGT GTG GAG GTG Leu Glu Val Ala Leu Phe Arg Ala Leu Glu Ala Arg Gly Val Glu Val 1685 1690 1695			5443
55	TCG GTG GTG TTG GGT CAT TCG GTG GGG GAG GTG GCT GCG TAT GTG Ser Val Val Leu Gly His Ser Val Gly Glu Val Ala Ala Ala Tyr Val			5491

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	1700	1705	1710		
5	GGC GGG GTG TTG TCG TTG GGT GAT GCG GTG CCG TTG GTG GTG GCG CGG Ala Gly Val Leu Ser Leu Gly Asp Ala Val Arg Leu Val Val Ala Arg 1715	1720	1725	1730	5539
10	GGT GGG TTG ATG GGT GGG TTG CCG GTG GGT GGG GGG ATG TGG TCG GTG Gly Gly Leu Met Gly Gly Leu Pro Val Gly Gly Met Trp Ser Val 1735	1740	1745		5587
15	GGG GCG TCG GAG TCG GTG GTG CCG GGG GTT GTT GAG GGG TTG GGG GAG Gly Ala Ser Glu Ser Val Val Arg Gly Val Val Glu Gly Leu Gly Glu 1750	1755	1760		5635
20	TGG GTG TCG GTT GCG GCG GTG AAT GGG CCG CGG TCG GTG GTG TTG TCG Trp Val Ser Val Ala Ala Val Asn Gly Pro Arg Ser Val Val Leu Ser 1765	1770	1775		5683
25	GGT GAT GTG GGT GTG CTG GAG TCG GTG GTT GCC TCG CTG ATG GGG GAT Gly Asp Val Gly Val Leu Glu Ser Val Val Ala Ser Leu Met Gly Asp 1780	1785	1790		5731
30	GGG GTG GAG TGC CCG CGG TTG GAT GTG TCG CAT GGG TTT CAT TCG GTG Gly Val Glu Cys Arg Arg Leu Asp Val Ser His Gly Phe His Ser Val 1795	1800	1805	1810	5779
35	TTG ATG GAG CCG GTG TTG GGG GAG TTC CCG GGG GTT GTG GAG TCG TTG Leu Met Glu Pro Val Leu Gly Glu Phe Arg Gly Val Val Glu Ser Leu 1815	1820	1825		5827
40	GAG TTC GGT CGG GTG CGG CCG GGT GTG GTG GTG TCG GGT GTG TCG Glu Phe Gly Arg Val Arg Pro Gly Val Val Val Ser Gly Val Ser 1830	1835	1840		5875
45	GGT GGG GTG GTG GGT TCG GGG GAG TTG GGG GAT CCG GGG TAT TGG GTG Gly Gly Val Val Gly Ser Gly Glu Leu Gly Asp Pro Gly Tyr Trp Val 1845	1850	1855		5923
50	CGT CAT GCG CGG GAG GCG GTG CGT TTC GCG GAT GGG GTG GGG GTG GTG Arg His Ala Arg Glu Ala Val Arg Phe Ala Asp Gly Val Gly Val Val 1860	1865	1870		5971
55	CGT GGT CTG GGT GTG GGG ACG TTG GTG GAG GTG GGT CCG CAT GGG GTG Arg Gly Leu Gly Val Gly Thr Leu Val Glu Val Gly Pro His Gly Val 1875	1880	1885	1890	6019
60	CTG ACG GGG ATG GCG GGT GAG TGC CTG GGG GCC GGT GAT GAT GTG GTG Leu Thr Gly Met Ala Gly Glu Cys Leu Gly Ala Gly Asp Asp Val Val 1895	1900	1905		6067
65	GTG GTG CCG GCG ATG CGG CGG GGC CGT GCG GAG CGG GAG GTG GTG TTC GAG Val Val Pro Ala Met Arg Arg Gly Arg Ala Glu Arg Glu Val Phe Glu 1910	1915	1920		6115
70	GCG GCG CTG GCG ACG GTG TTC ACC CGG GAC GCC GGC CTG GAC GCC ACG Ala Ala Leu Ala Thr Val Phe Thr Arg Asp Ala Gly Leu Asp Ala Thr 1925	1930	1935		6163
75	GCA CTC CAC ACC GGG AGC ACC GGC CGG CGC ATC GAC CTC CCC ACC TAC Ala Leu His Thr Gly Ser Thr Gly Arg Arg Ile Asp Leu Pro Thr Tyr				6211

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	1940	1945	1950	
5	CCC TTC CAA CGC GAC CGC TAC TGG CTG GAC CCC GTT CGC ACC GCC GTG Pro Phe Gln Arg Asp Arg Tyr Trp Leu Asp Pro Val Arg Thr Ala Val 1955 1960 1965 1970			6259
	ACC GGC GTC GAG CCC GCC GGC TCG CCG GCG GAC GCT CGG GCC ACT GAG Thr Gly Val Glu Pro Ala Gly Ser Pro Ala Asp Ala Arg Ala Thr Glu 1975 1980 1985			6307
10	CGG GGA CGG TCG ACG ACG GCC GGG ATC CGC TAC CGC GTC GCT TGG CAG Arg Gly Arg Ser Thr Thr Ala Gly Ile Arg Tyr Arg Val Ala Trp Gln 1990 1995 2000			6355
15	CCG GCC GTC GTC GAC CGC GGC AAC CCC GGG CCT GCC GGT CAT GTG CTG Pro Ala Val Val Asp Arg Gly Asn Pro Gly Pro Ala Gly His Val Leu 2005 2010 2015			6403
20	CTT CTG GCC CCG GAC GAG GAC ACG GCC GAC TCC GGA CTC GCC CCC GCG Leu Leu Ala Pro Asp Glu Asp Thr Ala Asp Ser Gly Leu Ala Pro Ala 2020 2025 2030			6451
	ATC GCA CGT GAA CTC GCC GTG CGC GGG GCC GAG GTC CAC ACC GTC GCC Ile Ala Arg Glu Leu Ala Val Arg Gly Ala Glu Val His Thr Val Ala 2035 2040 2045 2050			6499
25	GTC CCG GTC GGT ACA GGC CGG GAG GCA GCC GGG GAC CTG TTG CGG GCC Val Pro Val Gly Thr Gly Arg Glu Ala Ala Gly Asp Leu Leu Arg Ala 2055 2060 2065			6547
30	GCC GGT GAC CGT GCC GCC CGC ACC CGA GTT CTG TGG CTC GCC CCG Ala Gly Asp Gly Ala Ala Arg Ser Thr Arg Val Leu Trp Leu Ala Pro 2070 2075 2080			6595
	GCC GAG CCG GAC GCG GCC GAC GCC GTC GCC CTC GTC CAG GCG CTG GGC Ala Glu Pro Asp Ala Ala Asp Ala Val Ala Leu Val Gln Ala Leu Gly 2085 2090 2095			6643
35	GAG GCG GTA CCC GAA GCC CCG CTC TGG ATC ACC ACC CGT GAG GCG GCG Glu Ala Val Pro Glu Ala Pro Leu Trp Ile Thr Thr Arg Glu Ala Ala 2100 2105 2110			6691
40	GCC GTG CGG CCG GAC GAG ACC CCT TCC GTC GGG GGC GCT CAG CTG TGG Ala Val Arg Pro Asp Glu Thr Pro Ser Val Gly Ala Gln Leu Trp 2115 2120 2125 2130			6739
45	GGA CTC GGA CAG GTC GCC GCG CTC GAA CTG GGG CGG CGC TGG GGC GGC Gly Leu Gly Gln Val Ala Ala Leu Glu Leu Gly Arg Arg Trp Gly Gly 2135 2140 2145			6787
	TTG GCG GAC CTG CCC GGG AGT GCG TCG CCC GCG GTG CTC CGT ACG TTC Leu Ala Asp Leu Pro Gly Ser Ala Ser Pro Ala Val Leu Arg Thr Phe 2150 2155 2160			6835
50	GTC GGG GCG CTG CTC GCC GGG GGA GAG AAC CAG TTC GCG GTA CGG CCC Val Gly Ala Leu Leu Ala Gly Gly Glu Asn Gln Phe Ala Val Arg Pro 2165 2170 2175			6883
55	TCC GGC GTC CAT GTC CGC CGT GTG GTT CCC GCG CCC GTC CCC GTC CCG Ser Gly Val His Val Arg Arg Val Val Pro Ala Pro Val Pro Val Pro			6931

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	2180	2185	2190	
5	GCC TCC GCT CGC ACC GTC ACC ACG GCC CCC GCC ACC GCC GTC CGC GAG Ala Ser Ala Arg Thr Val Thr Ala Pro Ala Thr Ala Val Gly Glu 2195 2200 2205 2210			6979
	GAC GCA CGG AAC GAC ACC TCG GAC GTG GTC GTG CCG GAC GAC CGG TGG Asp Ala Arg Asn Asp Thr Ser Asp Val Val Val Pro Asp Asp Arg Trp 2215 2220 2225			7027
10	TCC TCC GGC ACC GTA CTG ATC ACC GGG GGC ACC GGT GCC CTG GGT GCG Ser Ser Gly Thr Val Leu Ile Thr Gly Gly Thr Gly Ala Leu Gly Ala 2230 2235 2240			7075
15	CAG GTC GCC CGC AGG CTC GCC CGG TCG GGC GCC GCG CGT CTG CTC CTG Gln Val Ala Arg Arg Leu Ala Arg Ser Gly Ala Ala Arg Leu Leu Leu 2245 2250 2255			7123
20	GTG GGC CGG CGC GGC GCG GCC GGC CCC GGA GTG GGC GAA CTC GTC GAG Val Gly Arg Arg Gly Ala Ala Gly Pro Gly Val Gly Glu Leu Val Glu 2260 2265 2270			7171
	GAG CTG ACG GCG CTC GGT TCC GAA GTG GCC GTC GAG GCC TGC GAC GTC Glu Leu Thr Ala Leu Gly Ser Glu Val Ala Val Glu Ala Cys Asp Val 2275 2280 2285 2290			7219
25	GCC GAC CGG GAC GCA CTG GCC GCG CTC CTC GCG GGC CTC CCC GAG GAG Ala Asp Arg Asp Ala Leu Ala Leu Leu Ala Gly Leu Pro Glu Glu 2295 2300 2305			7267
30	CGG CCC CTC GTC GCC GTA CTG CAC GCG GCA GGT GTG CTC GAC GAC GGT Arg Pro Leu Val Ala Val Leu His Ala Ala Gly Val Leu Asp Asp Gly 2310 2315 2320			7315
	GTG CTC GAC TCG CTC ACC TCC GAC CGG GTG GAC GCC GTA CTG CGG GAC Val Leu Asp Ser Leu Thr Ser Asp Arg Val Asp Ala Val Leu Arg Asp 2325 2330 2335			7363
35	AAG GTC ACC GCC CGC CGT CAC CTG GAC GAG CTG ACC GCG GAC CTT CCG Lys Val Thr Ala Ala Arg His Leu Asp Glu Leu Thr Ala Asp Leu Pro 2340 2345 2350			7411
40	CTC GAC GCC TTC GTG CTC TTC TCC ATC GTC GGC GTG TGG GGC AAC Leu Asp Ala Phe Val Leu Phe Ser Ser Ile Val Gly Val Trp Gly Asn 2355 2360 2365 2370			7459
	GGA GGG CAG GCC GTC TAC GCG GCC AAC GCC GCG CTC GAC GCC CTG Gly Gly Gln Ala Val Tyr Ala Ala Ala Asn Ala Ala Leu Asp Ala Leu 2375 2380 2385			7507
45	GCG CAG CGG CGC CGG GCC AGG GGA GCC CGT GCC GCC TCG ATC GCC TGG Ala Gln Arg Arg Ala Arg Gly Ala Arg Ala Ala Ser Ile Ala Trp 2390 2395 2400			7555
50	GGG CCG TGG GCC GGT GCC GGA ATG GCC TCC GGA ACG GCG GCG AAG TCC Gly Pro Trp Ala Gly Ala Gly Met Ala Ser Gly Thr Ala Ala Lys Ser 2405 2410 2415			7603
55	TTC GAA CGG GAC GGC GTC ACG GCC CTG GAC CCC GAG CGC GCG CTC GAC Phe Glu Arg Asp Gly Val Thr Ala Leu Asp Pro Glu Arg Ala Leu Asp			7651

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	2420	2425	2430	
5	GTC CTC GAC GAC GTG GTG GCC GGC GGG ACC TCT GCC GCA GGG ACG Val Leu Asp Asp Val Val Gly Ala Gly Gly Thr Ser Ala Ala Gly Thr 2435 2440 2445 2450			7699
	CAC GCG GCC GGC GAG AGC TCC CTG CTC GTC GCC GAC GTG GAC TGG GAG His Ala Ala Gly Glu Ser Ser Leu Leu Val Ala Asp Val Asp Trp Glu 2455 2460 2465			7747
10	ACC TTC GTC GGG CGT TCG GTC ACC CGC CGT ACC TGG TCG CTC TTC GAC Thr Phe Val Gly Arg Ser Val Thr Arg Arg Thr Trp Ser Leu Phe Asp 2470 2475 2480			7795
15	GCC GTC TCC GCC CGT TCG GCG CGT GCC CAT GCC GCG GAC GAC Gly Val Ser Ala Ala Arg Ser Ala Arg Ala Gly His Ala Ala Asp Asp 2485 2490 2495			7843
20	CGT GCC GCT CTC ACC CCA GGG ACG CGG CCG GGC GAC GGC GCA CCG GGC Arg Ala Ala Leu Thr Pro Gly Thr Arg Pro Gly Asp Gly Ala Pro Gly 2500 2505 2510			7891
	GGG AGC GGA CAG GAC GGG GGC GAG GGC CGG CCG TGG CTC TCC GTC GGC Gly Ser Gly Gln Asp Gly Glu Gly Arg Pro Trp Leu Ser Val Gly 2515 2520 2525 2530			7939
25	CCC TCG CCG GCG GAA CGC CGT CGT GCT CTG CTC ACG CTT GTG CGC TCG Pro Ser Pro Ala Glu Arg Arg Ala Leu Leu Thr Leu Val Arg Ser 2535 2540 2545			7987
30	GAG GCC GCC GGG ATC CTG CGC CAC GCC TCG GCC GAC GCG GTC GAC CCG Glu Ala Ala Gly Ile Leu Arg His Ala Ser Ala Asp Ala Val Asp Pro 2550 2555 2560			8035
	GAG CTG GCC TTC CGG TCC GCC GGG TTC GAC TCC CTC ACC GTT CTC GAA Glu Leu Ala Phe Arg Ser Ala Gly Phe Asp Ser Leu Thr Val Leu Glu 2565 2570 2575			8083
35	CTG CGT AAC CGC CTG ACC GCT GCC ACC GGC CTG AAC CTG CCG AAC ACG Leu Arg Asn Arg Leu Thr Ala Ala Thr Gly Leu Asn Leu Pro Asn Thr 2580 2585 2590			8131
40	CTG CTC TTC GAC CAC CCG ACC CCC CTC TCG CTC GCC TCC CAC CTG CAC Leu Leu Phe Asp His Pro Thr Pro Leu Ser Leu Ala Ser His Leu His 2595 2600 2605 2610			8179
	GAC GAA CTG TTC GGT CCC GAC AGC GAG GCG GAG CCG GCA GCG GCC GGC Asp Glu Leu Phe Gly Pro Asp Ser Glu Ala Glu Pro Ala Ala Ala 2615 2620 2625			8227
45	CCC ACG CCG GTC ATG GCC GAC GAG CGT GAG CCG ATC GCG ATC GTG GGC Pro Thr Pro Val Met Ala Asp Glu Arg Glu Pro Ile Ala Ile Val Gly 2630 2635 2640			8275
50	ATG GCG TGC CGT TAC CCG GGC GGT GTG GCG TCG CCG GAC GAC CTG TGG Met Ala Cys Arg Tyr Pro Gly Gly Val Ala Ser Pro Asp Asp Leu Trp 2645 2650 2655			8323
55	GAC CTG GTG GCC GGT GAC GGG CAC ACG CTC TCC CCG TTC CCG GCC GAC Asp Leu Val Ala Gly Asp Gly His Thr Leu Ser Pro Phe Pro Ala Asp			8371

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	2660	2665	2670	
5	CGT GGC TGG GAC GTC GAG GGG CTG TAC GAC CCG GAG CCG GGG GTG CCG Arg Gly Trp Asp Val Glu Gly Leu Tyr Asp Pro Glu Pro Gly Val Pro 2675 2680 2685 2690			8419
	Gly Lys Ser Tyr Val Arg Glu Gly Phe Leu Arg Ser Ala Ala Glu 2695 2700 2705			8467
10	TTC GAC GCG GAG TTC TTC GGG ATA TCG CCG CGC GAG GCC ACG GCC ATG Phe Asp Ala Glu Phe Gly Ile Ser Pro Arg Glu Ala Thr Ala Met 2710 2715 2720			8515
15	GAC CCG CAG CAG CGG TTG CTG CTG GAG ACG TCG TGG GAG GCG CTG GAG Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr Ser Trp Glu Ala Leu Glu 2725 2730 2735			8563
20	CGG GCC GGC ATC GTT CCG GAC TCG CTG CGC GGC ACC CGG ACC GGT GTC Arg Ala Gly Ile Val Pro Asp Ser Leu Arg Gly Thr Arg Thr Gly Val 2740 2745 2750			8611
	TTC AGC GGC ATC TCC CAG CAG GAC TAC GCG ACC CAG CTG GGG GAC GCC Phe Ser Gly Ile Ser Gln Gln Asp Tyr Ala Thr Gln Leu Gly Asp Ala 2755 2760 2765 2770			8659
25	GCC GAC ACC TAC GGC GGG CAT GTG CTC ACG GGG ACC CTC GGC AGT GTG Ala Asp Thr Tyr Gly Gly His Val Leu Thr Gly Thr Leu Gly Ser Val 2775 2780 2785			8707
30	ATC TCC GGT CGG GTT GCC TAT GCG TTG GGG TTG GAG GGG CCG GCG CTG Ile Ser Gly Arg Val Ala Tyr Ala Leu Gly Leu Glu Gly Pro Ala Leu 2790 2795 2800			8755
	ACG GTG GAC ACG GCG TGT TCG TCG TTG GTG GCG TTG CAT CTG GCG Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala 2805 2810 2815			8803
35	GTG CAG TCG TTG CGG CGG GGT GAG TGT GAT CTG GCG TTG GCC GGT GGG Val Gln Ser Leu Arg Arg Gly Glu Cys Asp Leu Ala Leu Ala Gly Gly 2820 2825 2830			8851
40	GTG ACG GTG ATG GCG ACG CCG ACG GTG TTC GTG GAG TTC TCG CGG CAG Val Thr Val Met Ala Thr Pro Thr Val Phe Val Glu Phe Ser Arg Gln 2835 2840 2845 2850			8899
45	CGG GGG CTG GCG GCG GAC GGG CGG TGC AAG GCG TTC GCG GAG GGT GCG Arg Gly Leu Ala Ala Asp Gly Arg Cys Lys Ala Phe Ala Glu Gly Ala 2855 2860 2865			8947
	GAC GGG ACG GCG TGG GCG GAG GGT GTG GGT GTG CTG CTG GTG GAG CGG Asp Gly Thr Ala Trp Ala Glu Gly Val Gly Val Leu Leu Val Glu Arg 2870 2875 2880			8995
50	CTT TCC GAC GCG CGC CGC AAC CGT CAT CGG GTG CTG GCG GTG GTG CGG Leu Ser Asp Ala Arg Arg Asn Gly His Arg Val Leu Ala Val Val Arg 2885 2890 2895			9043
55	GGC AGT GCG GTC AAT CAG GAC GGT GCG AGC AAT GGG CTG ACG GCG CCG Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro			9091

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	2900	2905	2910	
5	AGT GGT CCG GCG CAG CAG CGG GTG ATC CGT GAG GCG CTG GCT GAT GCG Ser Gly Pro Ala Gln Gln Arg Val Ile Arg Glu Ala Leu Ala Asp Ala 2915 2920 2925 2930			9139
	Gly			
	Gly Leu Val Pro Ala Asp Val Asp Val Val Glu Ala His Gly Thr Gly 2935 2940 2945			9187
10	ACG GCG CTG GGT GAT CCG ATC GAG GCG GGT GCG CTG CTG GCC ACG TAC Thr Ala Leu Gly Asp Pro Ile Glu Ala Gly Ala Leu Leu Ala Thr Tyr 2950 2955 2960			9235
	Gly			
15	GGG CGG GAG CGG GTC GGC GAT CCG TTG TGG CTC GGG TCG TTG AAG TCG Gly Arg Glu Arg Val Gly Asp Pro Leu Trp Leu Gly Ser Leu Lys Ser 2965 2970 2975			9283
	AAC			
	ATC GGG CAT GCG CAG GCG GCT GCG GGT GTG GGT GTG ATC AAG Asn Ile Gly His Ala Gln Ala Ala Gly Val Gly Gly Val Ile Lys 2980 2985 2990			9331
20	GTG GTG CAG GGG ATG CGG CAT GGG TCG TTG CCG CGG ACG CTG CAT GTG Val Val Gln Gly Met Arg His Gly Ser Leu Pro Arg Thr Leu His Val 2995 3000 3005 3010			9379
	Val			
25	GAT GCG CCG TCG TCG AAG GTG GAG TGG GCT TCG GGT GCG GTG GAG CTG Asp Ala Pro Ser Ser Lys Val Glu Trp Ala Ser Gly Ala Val Glu Leu 3015 3020 3025			9427
	Asp			
30	CTG ACC GAG ACC CGG TCG TGG CCG CGG CGG GTG GAG CGG CGG CGG CGG Leu Thr Glu Thr Arg Ser Trp Pro Arg Arg Val Glu Arg Val Arg Arg 3030 3035 3040			9475
	Leu			
	GCC GCG GTG TCG GCG TTC GGG GTG AGC GGG ACC AAC GCC CAT GTG GTC Ala Ala Val Ser Ala Phe Gly Val Ser Gly Thr Asn Ala His Val Val 3045 3050 3055			9523
35				
	CTG GAG GAA GCG CCG GCG GAG GCC GGG AGC GAG CAC GGG GAC GGC CCT Leu Glu Glu Ala Pro Ala Glu Ala Gly Ser Glu His Gly Asp Gly Pro 3060 3065 3070			9571
	Leu			
40	GAA CCT GAG CGG CCC GAC GCG GTG ACG GGT CCG TTG TCG TGG GTG CTT Glu Pro Glu Arg Pro Asp Ala Val Thr Gly Pro Leu Ser Trp Val Leu 3075 3080 3085 3090			9619
	Glu			
45	TCT GCG CGG TCG GAG GGG GCG TTG CGG GCG CAG GCG GTG CGG TTG CGT Ser Ala Arg Ser Glu Gly Ala Leu Arg Ala Gln Ala Val Arg Leu Arg 3095 3100 3105			9667
	Ser			
	GAG TGT GTG GAG CGG GTG GGT GCG GAT CCG CGG GAT GTG GCG GGG TCG Glu Cys Val Glu Arg Val Gly Ala Asp Pro Arg Asp Val Ala Gly Ser 3110 3115 3120			9715
50				
	TTG GTG GTG TCG CGT GCG TCG TTC CGT GAC CGT GCG GTG GTG GTG GGC Leu Val Val Ser Arg Ala Ser Phe Gly Glu Arg Ala Val Val Val Gly 3125 3130 3135			9763
	Leu			
55	CGG CGG CGT GAG GAG TTG CTG GCG GGT CTG GAT GTG GTG GCT GCC GGG Arg Gly Arg Glu Glu Leu Leu Ala Gly Leu Asp Val Val Ala Ala Gly			9811

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	3140	3145	3150	
5	GCT CCT GTG GGT GTG TCT TCG GGG GCC GGT GCT GTG GTG CGG GGG AGT Ala Pro Val Gly Val Ser Ser Gly Ala Gly Ala Val Val Arg Gly Ser 3155 3160 3165 3170			9859
	GCG GTG CGG GGT CGT GGG GTG GGG GTG TTG TTC ACG GGT CAG GGT GCG Ala Val Arg Gly Arg Gly Val Gly Val Leu Phe Thr Gly Gln Gly Ala 3175 3180 3185			9907
10	CAG TGG GTT GGT ATG GGG CGT GGG TTG TAT GCG GGG GGT GGG GTG TTT Gln Trp Val Gly Met Gly Arg Gly Leu Tyr Ala Gly Gly Val Phe 3190 3195 3200			9955
15	GCG GAG GTG CTG GAT GAG GTG TTG TCG GTG GTG GGG GAG GTG GAT GGT Ala Glu Val Leu Asp Glu Val Leu Ser Val Val Gly Glu Val Asp Gly 3205 3210 3215			10003
20	CGG TCG TTG CGG GAT GTG ATG TTC GCG GAT GCT GAC TCG GTT TTG GGT Arg Ser Leu Arg Asp Val Met Phe Ala Asp Ala Asp Ser Val Leu Gly 3220 3225 3230			10051
	GGG TTG TTG GGT CGG ACG GAG TTT GCT CAG CCT GCG TTG TTT GCG TTG Gly Leu Leu Gly Arg Thr Glu Phe Ala Gln Pro Ala Leu Phe Ala Leu 3235 3240 3245 3250			10099
25	GAG GTG GCG TTG TTC CGG GCG TTG GAG GCT CGG GGT GTG GAG GTG TCG Glu Val Ala Leu Phe Arg Ala Leu Glu Ala Arg Gly Val Glu Val Ser 3255 3260 3265			10147
30	GTG GTG TTG GGT CAT TCG GTG GGG GAG GTG GCT GCT GCG TAT GTG GCG Val Val Leu Gly His Ser Val Gly Glu Val Ala Ala Ala Tyr Val Ala 3270 3275 3280			10195
	GGG GTG TTG TCG TTG GGT GAT GCG GTG CGG TTG GTG GTG GCG CGG CGT Gly Val Leu Ser Leu Gly Asp Ala Val Arg Leu Val Val Ala Arg Gly 3285 3290 3295			10243
35	GGG TTG ATG GGT GGG TTG CCG GTG GGT GGG GGG ATG TGG TCG GTG GGG Gly Leu Met Gly Gly Leu Pro Val Gly Gly Met Trp Ser Val Gly 3300 3305 3310			10291
40	GCG TCG GAG TCG GTG CGG GGG GTT GTT GAG GGG TTG GGG GAG TGG Ala Ser Glu Ser Val Val Arg Gly Val Val Glu Gly Leu Gly Glu Trp 3315 3320 3325 3330			10339
45	GTG TCG GTT GCG GCG GTG AAT GGG CCG CGG TCG GTG GTG TTG TCG GGT Val Ser Val Ala Ala Val Asn Gly Pro Arg Ser Val Val Leu Ser Gly 3335 3340 3345			10387
	GAT GTG GGT GTG CTG GAG TCG GTG GTT GTC ACG CTG ATG GGG GAT GGG Asp Val Gly Val Leu Glu Ser Val Val Val Thr Leu Met Gly Asp Gly 3350 3355 3360			10435
50	GTG GAG TGC CGG CGG TTG GAT GTG TCG CAT GGG TTT CAT TCG GTG TTG Val Glu Cys Arg Arg Leu Asp Val Ser His Gly Phe His Ser Val Leu 3365 3370 3375			10483
55	ATG GAG CCG GTG TTG GGG GAG TTC CGG GGG GTT GTG GAG TCG TTG GAG Met Glu Pro Val Leu Gly Glu Phe Arg Gly Val Val Glu Ser Leu Glu			10531

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	3380	3385	3390	
5	TTC GGT CGG GTG CGG CGG GGT GTG GTG GTG GTG TCG GGT GTG TCG GGT Phe Gly Arg Val Arg Pro Gly Val Val Val Ser Gly Val Ser Gly 3395 3400 3405 3410			10579
	Gly Val Val Gly Ser Gly Glu Leu Gly Asp Pro Gly Tyr Trp Val Arg 3415 3420 3425			10627
10	CAT GCG CGG GAG GCG GTG CGT TTC GCG GAT GGG GTG GGG GTG GTG CGT His Ala Arg Ala Val Arg Phe Ala Asp Gly Val Gly Val Val Arg 3430 3435 3440			10675
15	GGT CTG GGT GTG GGG ACG TTG GTG GAG GTG GGT CCG CAT GGG GTG CTG Gly Leu Gly Val Gly Thr Leu Val Glu Val Gly Pro His Gly Val Leu 3445 3450 3455			10723
20	ACG CGG ATG CGC GGT CAG TGC CTG GAG GCC GGT GAT GAT GTG GTG GTG Thr Gly Met Ala Gly Gln Cys Leu Glu Ala Gly Asp Asp Val Val Val 3460 3465 3470			10771
	GTG CCG GCG ATG CGG CGG GGC CGT CCG GAG CGG GAG GTG TTC GAG GCG Val Pro Ala Met Arg Arg Gly Arg Pro Glu Arg Glu Val Phe Glu Ala 3475 3480 3485 3490			10819
25	GCG CTG GCG ACC GTG TTC ACC CGG GAC GCC GGC CTC GAC GCC ACG ACA Ala Leu Ala Thr Val Phe Thr Arg Asp Ala Gly Leu Asp Ala Thr Thr 3495 3500 3505			10867
30	CTC CAC ACC GGG AGC ACC GGC CGA CGC ATC GAC CTC CCC ACC TAC CCC Leu His Thr Gly Ser Thr Gly Arg Arg Ile Asp Leu Pro Thr Tyr Pro 3510 3515 3520			10915
	TTC CAA CAC AAC CGC TAC TGG GCA ACC GGC TCA GTG ACC GGT GCG ACC Phe Gln His Asn Arg Tyr Trp Ala Thr Gly Ser Val Thr Gly Ala Thr 3525 3530 3535			10963
35	GGC ACC TCG GCA GCC GCG CGC TTC GGC CTG GAG TGG AAG GAC CAC CCC Gly Thr Ser Ala Ala Arg Phe Gly Leu Glu Trp Lys Asp His Pro 3540 3545 3550			11011
40	TTC CTC AGC GGC GCC ACG CCG ATA GCC GGC TCC GGC GCG CTG CTC CTC Phe Leu Ser Gly Ala Thr Pro Ile Ala Gly Ser Gly Ala Leu Leu Leu 3555 3560 3565 3570			11059
45	ACC GGC AGG GTG GGG CTC GCT GCC CAC CCG TGG CTG GCC GAC CAC GCC Thr Gly Arg Val Gly Leu Ala Ala His Pro Trp Leu Ala Asp His Ala 3575 3580 3585			11107
	ATC TCC GGC ACG GTG CTG CTC CCC GGA ACG GCG ATC GCC GAC CTG CTG Ile Ser Gly Thr Val Leu Leu Pro Gly Thr Ala Ile Ala Asp Leu Leu 3590 3595 3600			11155
50	CTG CGG GCG GTC GAG GAG GTC GGC GCC GGA GGG GTC GAG GAA CTG ACG Leu Arg Ala Val Glu Glu Val Gly Ala Gly Gly Val Glu Glu Leu Thr 3605 3610 3615			11203
55	CTC CAT GAG CCC CTG CTC CTC CCC GAG CGA GGC GGC CTG CAC GTC CAG Leu His Glu Pro Leu Leu Pro Glu Arg Gly Gly Leu His Val Gln			11251

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	3620	3625	3630	
5	GTG CTG GTC GAG GCG GCC GAC GAG CAG GGA CGG CGT GCC GTG GCA GTC Val Leu Val Glu Ala Ala Asp Glu Gln Gly Arg Arg Ala Val Ala Val 3635 3640 3645 3650			11299
	GCC GCA CGC CCG GAG GGC CCT GGG CGG GAC GGT GAG GAA CAG GAG TGG Ala Ala Arg Pro Glu Gly Pro Gly Arg Asp Gly Glu Glu Gln Glu Trp 3655 3660 3665			11347
10	ACC CGG CAC GCG GAA GGC GTG CTC ACC TCC ACC GAG ACG GCC GTT CCG Thr Arg His Ala Glu Gly Val Leu Thr Ser Thr Glu Thr Ala Val Pro 3670 3675 3680			11395
15	GAC ATG GGC TGG GCC GCC GGG GCC TGG CCG CCC GGT GCC GAG CCG Asp Met Gly Trp Ala Ala Gly Ala Trp Pro Pro Pro Gly Ala Glu Pro 3685 3690 3695			11443
	ATC GAC GTC GAG GAG CTG TAC GAC GCG TTC GCC GCG GAC GGC TAC GGC Ile Asp Val Glu Glu Leu Tyr Asp Ala Phe Ala Ala Asp Gly Tyr Gly 3700 3705 3710			11491
20	TAC GGC CCG GCC TTC ACC GCA CTG TCC GGC GTG TGG CGT CTC GGC GAC Tyr Gly Pro Ala Phe Thr Ala Leu Ser Gly Val Trp Arg Leu Gly Asp 3715 3720 3725 3730			11539
25	GAA CTC TTC GCC GAG GTG CGG CGG CCC GCG GGG GGC GCG GGC ACG ACC Glu Leu Phe Ala Glu Val Arg Arg Pro Ala Gly Gly Ala Gly Thr Thr 3735 3740 3745			11587
30	GGT GAC GGT TTC CCC GTC CAC CCC GCA CTC TTC GAT GCG GGC CTC CAC Gly Asp Gly Phe Gly Val His Pro Ala Leu Phe Asp Ala Ala Leu His 3750 3755 3760			11635
	CCG TGG CGC GCC GGC GGG CTG CTG CCC GAC ACG GGC GGC ACC ACC TGG Pro Trp Arg Ala Gly Gly Leu Leu Pro Asp Thr Gly Gly Thr Thr Trp 3765 3770 3775			11683
35	GCG CCG TTC TCC TGG CAG GGC ATC GCG CTC CAC ACC ACC GGA GCC GAG Ala Pro Phe Ser Trp Gln Gly Ile Ala Leu His Thr Thr Gly Ala Glu 3780 3785 3790			11731
40	ACG CTC CGC CTC AGA CTG GCC CCT GCG GCC GGC ACC CCG ACC GAG TCG GCC Thr Leu Arg Val Arg Leu Ala Pro Ala Ala Gly Gly Thr Glu Ser Ala 3795 3800 3805 3810			11779
45	TTC TCC GTA CAG GCC GGC GAC CCG GCG GGC ACC CCG GTC CTC ACC CTC Phe Ser Val Gln Ala Ala Asp Pro Ala Gly Thr Pro Val Leu Thr Leu 3815 3820 3825			11827
	GAC GCA CTG CTG CTC CGC CCG GTG ACC CTG GGG AGG GCC GAC GCG CCG Asp Ala Leu Leu Leu Arg Pro Val Thr Leu Gly Arg Ala Asp Ala Pro 3830 3835 3840			11875
50	CAA CCG CTG TAC CGC GTC GAC TGG CAG CCG GTC GGC CAG GGG ACC GAG Gln Pro Leu Tyr Arg Val Asp Trp Gln Pro Val Gly Gln Gly Thr Glu 3845 3850 3855			11923
55	GCC TCC CGC GCC CAG GGC TGG ACG GTG CTC GGG CAG GCC GCG GGC GAG Ala Ser Gly Ala Gln Gly Trp Thr Val Leu Gly Gln Ala Ala Glu			11971

	3860	3865	3870	
5	ACG GTC GCG CAG CCC GCC CAT GCG GAC CTC ACC GCC CTG CGT ACG Thr Val Ala Gln Pro Ala Ala His Ala Asp Leu Thr Ala Leu Arg Thr 3875 3880 3885 3890			12019
	GCT GTG GCC GCG GCG GGA ACA CCC GTG CCC CGG CTG GTG GTC GTG TCG Ala Val Ala Ala Ala Gly Thr Pro Val Pro Arg Leu Val Val Val Ser 3895 3900 3905			12067
10	CCG GTG GAC ACC CGG CTG GAC GAG GGG CCG GTG CTG GCG GAC GCC GAG Pro Val Asp Thr Arg Leu Asp Glu Gly Pro Val Leu Ala Asp Ala Glu 3910 3915 3920			12115
15	GCT CGG GCC CGT GCG GGT GAC GGC TGG GAC GAT CCC CTA CGT GTC Ala Arg Ala Arg Ala Gly Asp Gly Trp Asp Asp Asp Pro Leu Arg Val 3925 3930 3935			12163
20	GCC CTC GGG CGC GGC CTG ACC CTG GTC CGG GAG TGG GTC GAG GAC GAA Ala Leu Gly Arg Gly Leu Thr Leu Val Arg Glu Trp Val Glu Asp Glu 3940 3945 3950			12211
	CGG TTG GCG GAC TCC CGG CTC GTC GTC CTC ACC CGT GGC GCG GTG GCG Arg Leu Ala Asp Ser Arg Leu Val Val Leu Thr Arg Gly Ala Val Ala 3955 3960 3965 3970			12259
25	GCC GGT CCC GGC GAT GTG CCG GAC CTG ACA GGT GCG GCC CTG TGG GGG Ala Gly Pro Gly Asp Val Pro Asp Leu Thr Gly Ala Ala Leu Trp Gly 3975 3980 3985			12307
30	CTG CTC CGC TCC GCG CAG TCG GAG TAT CCG GAC CGC TTC ACC CTC ATC Leu Leu Arg Ser Ala Gln Ser Glu Tyr Pro Asp Arg Phe Thr Leu Ile 3990 3995 4000			12355
	GAC GTG GAC GAT TCC CCC GAG TCC CGT GCG GCT CTG CCC CGG GCT CTG Asp Val Asp Asp Ser Pro Glu Ser Arg Ala Ala Leu Pro Arg Ala Leu 4005 4010 4015			12403
35	GGA TCG GCC GAG CGA CAA CTC GCC CTG CGG ACG GGC GAC GTG CTG GCG Gly Ser Ala Glu Arg Gln Leu Ala Leu Arg Thr Gly Asp Val Leu Ala 4020 4025 4030			12451
40	CCG GCC CTG GTC CCG ATG GCC ACC CGG CCG GCG GAG ACC ACT CCA GCG Pro Ala Leu Val Pro Met Ala Thr Arg Pro Ala Glu Thr Thr Pro Ala 4035 4040 4045 4050			12499
45	ACG GCG GTC GCC TCG GCG ACA ACA CAG ACA CAG GTC ACC GCG CCC GCT Thr Ala Val Ala Ser Ala Thr Thr Gln Thr Gln Val Thr Ala Pro Ala 4055 4060 4065			12547
	CCC GAC GAC CCG GCT GCG GAT GCC GTG TTC GAC CCG GCG GGC ACC GTA Pro Asp Asp Pro Ala Ala Asp Ala Val Phe Asp Pro Ala Gly Thr Val 4070 4075 4080			12595
50	CTG ATC ACC GGC GGC ACC GGC GCC CTG GGA CGG CGT GTC GCC TCG CAC Leu Ile Thr Gly Gly Thr Gly Ala Leu Gly Arg Arg Val Ala Ser His 4085 4090 4095			12643
55	CTC GCG CGC CGG TAC GGC GTA CGC CAC ATG CTT CTG GTC AGC AGG CGT Leu Ala Arg Arg Tyr Gly Val Arg His Met Leu Leu Val Ser Arg Arg			12691

	4100	4105	4110	
5	GGA CCG GAC GCC CCC GAG GCC GGT CCC CTG GAA CGG GAA CTC GCC GGT Gly Pro Asp Ala Pro Glu Ala Gly Pro Leu Glu Arg Glu Leu Ala Gly 4115 4120 4125 4130			12739
	CTC GGA GTC ACC GCC ACC TTC CTG GCA TGC GAC CTC ACC GAC ATC GAG Leu Gly Val Thr Ala Thr Phe Leu Ala Cys Asp Leu Thr Asp Ile Glu 4135 4140 4145			12787
10	GCC GTA CGG AAG GCC GTC GCC GCG GTG CCG TCG GAC CAC CCG CTG ACC Ala Val Arg Lys Ala Val Ala Val Pro Ser Asp His Pro Leu Thr 4150 4155 4160			12835
15	GGT GTG GTG CAC ACC GCC GGC GTG CTG GAC GGC GCC CTG ACC GGC Gly Val Val His Thr Ala Gly Val Leu Asp Asp Gly Ala Leu Thr Gly 4165 4170 4175			12883
	CTG ACC CGG CAA CGC CTC GAC ACC GTG CTG CGG CCC AAG GCC GAC GCC Leu Thr Arg Gln Arg Leu Asp Thr Val Leu Arg Pro Lys Ala Asp Ala 4180 4185 4190			12931
20	GTG CGG AAC CTC CAC GAG GCG ACC CTC GAC CGG CCG CTG CGC GCG TTC Val Arg Asn Leu His Glu Ala Thr Leu Asp Arg Pro Leu Arg Ala Phe 4195 4200 4205 4210			12979
25	GTC CTG TTC TCC GCC GCC GGA CTC CTG GGC CGC CCC GGG CAG GCC Val Leu Phe Ser Ala Ala Ala Gly Leu Leu Gly Arg Pro Gly Gln Ala 4215 4220 4225			13027
30	TCC TAC GCC GCC AAC GCG GTC CTC GAC GCG CTC GCG GGA GCC CGC Ser Tyr Ala Ala Ala Asn Ala Val Leu Asp Ala Leu Ala Gly Ala Arg 4230 4235 4240			13075
	CGC GCG GCC GGA CTG CCC GCA GTG TCC CTG GCG TGG GGC CTG TGG GAC Arg Ala Ala Gly Leu Pro Ala Val Ser Leu Ala Trp Gly Leu Trp Asp 4245 4250 4255			13123
35	GAG CAG ACG CGC ATG GCA GGA GGC CTC GAC GAG ATG GCC CTG CGC GTG Glu Gln Thr Gly Met Ala Gly Gly Leu Asp Glu Met Ala Leu Arg Val 4260 4265 4270			13171
40	CTG CGC CGG GAC GGC ATC GCC GCG ATG CCT CCG GAG CAG GGG CTC GAA Leu Arg Arg Asp Gly Ile Ala Ala Met Pro Pro Glu Gln Gly Leu Glu 4275 4280 4285 4290			13219
45	CTG CTC GAC CTG GCC CTG ACC GGA CAC CGG GAC GGA CCC GCC GTC CTC Leu Leu Asp Leu Ala Leu Thr Gly His Arg Asp Gly Pro Ala Val Leu 4295 4300 4305			13267
	GTC CCC CTC CTC GAC GGC GCG GCC CTG CGC CGC ACG GCG AAG GAG Val Pro Leu Leu Asp Gly Ala Ala Leu Arg Arg Thr Ala Lys Glu 4310 4315 4320			13315
50	CGC GGC GCG GCC ACG ATG TCC CCC TTG CTG CGC GCC CTG CTG CCC GCC Arg Gly Ala Ala Thr Met Ser Pro Leu Leu Arg Ala Leu Leu Pro Ala 4325 4330 4335			13363
55	GCC CTG CGC CGC AGC GGT GGA GCC GGC GCC CCC GCG GCG GCC GAC CGG Ala Leu Arg Arg Ser Gly Gly Ala Gly Ala Pro Ala Ala Asp Arg			13411

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	4340	4345	4350	
5	CAC GGC AAG GAG GCG GAC CCC GGT GCG GGA CGC CTC GCA GGG ATG GTG His Gly Lys Glu Ala Asp Pro Gly Ala Gly Arg Leu Ala Gly Met Val 4355 4360 4365 4370			13459
	GCA CTC GAA GCG GCG GAG CGT TCC GCG GCC GTC CTT GAG CTG GTC ACC Ala Leu Glu Ala Ala Glu Arg Ser Ala Ala Val Leu Glu Leu Val Thr 4375 4380 4385			13507
10	GAA CAG GTC GCC GAG GTC CTC GGC TAC GCG TCG GCC GCG GAG ATC GAG Glu Gln Val Ala Glu Val Leu Gly Tyr Ala Ser Ala Ala Glu Ile Glu 4390 4395 4400			13555
15	CCC GAA CGA CCC TTC CCG GAG ATC GGC GTC GAC TCC CTG GCG GCG GTG Pro Glu Arg Pro Phe Arg Glu Ile Gly Val Asp Ser Leu Ala Ala Val 4405 4410 4415			13603
20	GAG CTG CGC AAC CGG CTC AGC CGT CTG GTC GGC CTG CGG TTG CCG ACC Glu Leu Arg Asn Arg Leu Ser Arg Leu Val Gly Leu Arg Leu Pro Thr 4420 4425 4430			13651
	ACG CTG TCC TTC GAC CAC CCC ACG CCG AAG GAC ATG GCG CAG CAC ATC Thr Leu Ser Phe Asp His Pro Thr Pro Lys Asp Met Ala Gln His Ile 4435 4440 4445 4450			13699
25	GAC GGG CAG CTC CCC CGC CCG GCC GGA GCC TCG CCC GCG GAC GCA GCG Asp Gly Gln Leu Pro Arg Pro Ala Gly Ala Ser Pro Ala Asp Ala Ala 4455 4460 4465			13747
30	CTG GAA GGG ATC GGC GAC CTC GCG CGG GCG GTC GCC CTG CTG GGC ACG Leu Glu Gly Ile Gly Asp Leu Ala Arg Ala Val Ala Leu Leu Gly Thr 4470 4475 4480			13795
	GGC GAC GCC CGC CGG GCC GAG GTA CGA GAG CAG CTC GTC GGA CTG CTG Gly Asp Ala Arg Arg Ala Glu Val Arg Glu Gln Leu Val Gly Leu Leu 4485 4490 4495			13843
35	GCC GCG CTC GAC CCA CCT GGG CGG ACG GGC ACC GCC GCA CCC GGC GTC Ala Ala Leu Asp Pro Pro Gly Arg Thr Gly Thr Ala Ala Pro Gly Val 4500 4505 4510			13891
40	CCC TCC GGT GCC GAT GGC GCG GAA CCG ACC GTG ACG GAC CGG CTC GAC Pro Ser Gly Ala Asp Gly Ala Glu Pro Thr Val Thr Asp Arg Leu Asp 4515 4520 4525 4530			13939
45	GAG GCG ACC GAC GAC GAG ATC TTC GCC TTC CTG GAC GAG CAG CTG TGA Glu Ala Thr Asp Asp Glu Ile Phe Ala Phe Leu Asp Glu Gln Leu * 4535 4540 4545			13987

(2) INFORMATION FOR SEQ ID NO:14:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4546 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
- 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ser Gly Glu Leu Ala Ile Ser Arg Ser Asp Asp Arg Ser Asp Ala
 1 5 10 15

Val Ala Val Val Gly Met Ala Cys Arg Phe Pro Gly Ala Pro Gly Ile
 20 25 30

Ala Glu Phe Trp Glu Leu Leu Arg Ser Gly Arg Gly Met Pro Thr Arg
 35 40 45

Gln Asp Asp Gly Thr Trp Arg Ala Ala Leu Glu Asp His Ala Gly Phe
 50 55 60

Asp Ala Gly Phe Phe Gly Met Asn Ala Arg Gln Ala Ala Ala Thr Asp
 65 70 75 80

Pro Gln His Arg Leu Met Leu Glu Leu Gly Trp Glu Ala Leu Glu Asp
 85 90 95

Ala Gly Ile Val Pro Gly Asp Leu Thr Gly Thr Asp Thr Gly Val Phe
 100 105 110

Ala Gly Val Ala Ser Asp Asp Tyr Ala Val Leu Thr Arg Arg Ser Ala
 115 120 125

Val Ser Ala Gly Gly Tyr Thr Ala Thr Gly Leu His Arg Ala Leu Ala
 130 135 140

Ala Asn Arg Leu Ser His Phe Leu Gly Leu Arg Gly Pro Ser Leu Val
 145 150 155 160

Val Asp Ser Ala Gln Ser Ala Ser Leu Val Ala Val Gln Leu Ala Cys
 165 170 175

Glu Ser Leu Arg Arg Gly Glu Thr Ser Leu Ala Val Ala Gly Gly Val
 180 185 190

Asn Leu Ile Leu Thr Glu Glu Ser Thr Thr Val Met Glu Arg Met Gly
 195 200 205

Ala Leu Ser Pro Asp Gly Arg Cys His Thr Phe Asp Ala Arg Ala Asn
 210 215 220

Gly Tyr Val Arg Gly Glu Gly Gly Ala Val Val Leu Lys Pro Leu
 225 230 235 240

Asp Ala Ala Leu Ala Asp Gly Asp Arg Val Tyr Cys Val Ile Lys Gly
 245 250 255

Gly Ala Val Asn Asn Asp Gly Gly Ala Ser Leu Thr Thr Pro Asp
 260 265 270

Arg Glu Ala Gln Glu Ala Val Leu Arg Gln Ala Tyr Arg Arg Ala Gly
 275 280 285

Val Ser Thr Gly Ala Val Arg Tyr Val Glu Leu His Gly Thr Gly Thr
 290 295 300

Arg Ala Gly Asp Pro Val Glu Ala Ala Leu Gly Ala Val Leu Gly

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	305	310	315	320
	Ala Gly Ala Asp Ser Gly Arg Ser Thr Pro Leu Ala Val Gly Ser Val			
5	325		330	335
	Lys Thr Asn Val Gly His Leu Glu Gly Ala Ala Gly Ile Val Gly Leu			
	340	345		350
10	Ile Lys Ala Thr Leu Cys Val Arg Lys Gly Glu Leu Val Pro Ser Leu			
	355	360	365	
	Asn Phe Ser Thr Pro Asn Pro Asp Ile Pro Leu Asp Asp Leu Arg Leu			
15	370	375	380	
	Arg Val Gln Thr Glu Arg Gln Glu Trp Asn Glu Glu Asp Asp Arg Pro			
	385	390	395	400
	Arg Val Ala Gly Val Ser Ser Phe Gly Met Gly Gly Thr Asn Val His			
	405	410		415
20	Leu Val Ile Ala Glu Ala Pro Ala Ala Gly Ser Ser Gly Ala Gly			
	420	425	430	
	Gly Ser Gly Ala Gly Ser Gly Ala Gly Ile Ser Ala Val Ser Gly Val			
	435	440	445	
25	Val Pro Val Val Val Ser Gly Arg Ser Arg Val Val Val Arg Glu Ala			
	450	455	460	
	Ala Gly Arg Leu Ala Glu Val Val Glu Ala Gly Gly Val Gly Leu Ala			
	465	470	475	480
30	Asp Val Ala Val Thr Met Ala Asp Arg Ser Arg Phe Gly Tyr Arg Ala			
	485	490	495	
	Val Val Leu Ala Arg Gly Glu Ala Glu Leu Ala Gly Arg Leu Arg Ala			
	500	505	510	
35	Leu Ala Gly Gly Asp Pro Asp Ala Gly Val Val Thr Gly Ala Val Leu			
	515	520	525	
	Asp Gly Gly Val Val Val Gly Ala Ala Pro Gly Gly Ala Gly Ala Ala			
40	530	535	540	
	Gly Gly Ala Gly Ala Ala Gly Gly Ala Gly Gly Gly Val Val Leu			
	545	550	555	560
45	Val Phe Pro Gly Gln Gly Thr Gln Trp Val Gly Met Gly Ala Gly Leu			
	565	570	575	
	Leu Gly Ser Ser Glu Val Phe Ala Ala Ser Met Arg Glu Cys Ala Arg			
	580	585	590	
50	Ala Leu Ser Val His Val Gly Trp Asp Leu Leu Glu Val Val Ser Gly			
	595	600	605	
	Gly Ala Gly Leu Glu Arg Val Asp Val Val Gln Pro Val Thr Trp Ala			
	610	615	620	
55	Val Met Val Ser Leu Ala Arg Tyr Trp Gln Ala Met Gly Val Asp Val			

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	625	630	635	640
	Ala Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala Thr Val			
5	645	650	655	
	Ala Gly Ala Leu Ser Leu Glu Asp Ala Ala Ala Val Val Ala Leu Arg			
	660	665	670	
10	Ala Gly Leu Ile Gly Arg Tyr Leu Ala Gly Arg Gly Ala Met Ala Ala			
	675	680	685	
	Val Pro Leu Pro Ala Gly Glu Val Glu Ala Gly Leu Ala Lys Trp Pro			
	690	695	700	
15	Gly Val Glu Val Ala Ala Val Asn Gly Pro Ala Ser Thr Val Val Ser			
	705	710	715	720
	Gly Asp Arg Arg Ala Val Ala Gly Tyr Val Ala Val Cys Gln Ala Glu			
	725	730	735	
20	Gly Val Gln Ala Arg Leu Ile Pro Val Asp Tyr Ala Ser His Ser Arg			
	740	745	750	
	His Val Glu Asp Leu Lys Gly Glu Leu Glu Arg Val Leu Ser Gly Ile			
	755	760	765	
25	Arg Pro Arg Ser Pro Arg Val Pro Val Cys Ser Thr Val Ala Gly Glu			
	770	775	780	
	Gln Pro Gly Glu Pro Val Phe Asp Ala Gly Tyr Trp Phe Arg Asn Leu			
	785	790	795	800
30	Arg Asn Arg Val Glu Phe Ser Ala Val Val Gly Gly Leu Leu Glu Glu			
	805	810	815	
	Gly His Arg Arg Phe Ile Glu Val Ser Ala His Pro Val Leu Val His			
	820	825	830	
35	Ala Ile Glu Gln Thr Ala Glu Ala Ala Asp Arg Ser Val His Ala Thr			
	835	840	845	
	Gly Thr Leu Arg Arg Gln Asp Asp Ser Pro His Arg Leu Leu Thr Ser			
40	850	855	860	
	Thr Ala Glu Ala Trp Ala His Gly Ala Thr Leu Thr Trp Asp Pro Ala			
	865	870	875	880
45	Leu Pro Pro Gly His Leu Thr Thr Leu Pro Thr Tyr Pro Phe Asn His			
	885	890	895	
	His His Tyr Trp Leu Asp Thr Ile Asp Gly Gly Gly Asp Asp Ala			
	900	905	910	
50	Thr Gln Glu Lys Glu Ser Gly Pro Leu Thr Arg Glu Leu Arg Gly Leu			
	915	920	925	
	Pro Ser Ser Gln Lys Gln Leu Gly Phe Leu Leu Asp Leu Val Cys Arg			
	930	935	940	
55	His Thr Ala Val Val Leu Gly Leu Asp Thr Ala Ala Glu Val Asp Pro			

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	945	950	955	960
	Asp Leu Ser Phe Lys Lys Gln Gly Ile Gln Ser Met Thr Gly Val Glu			
	965		970	975
5	Leu Arg Asn Arg Leu Leu Thr Glu Thr Gly Leu Ala Leu Pro Thr Thr			
	980		985	990
	Leu Val Tyr Asp Arg Pro Thr Pro Arg Ala Leu Ala Gln Phe Leu His			
10	995		1000	1005
	Thr Glu Leu Leu Asp Gly Ser Pro Ser Gly Ser Val Leu Ala Pro Ala			
	1010		1015	1020
15	Gln Lys Ser Phe Glu Ala Gly Gly Pro Gly Val Leu Ser Ser Ala Ala			
	1025		1030	1035
	Val Gly Val Ser Asp Ala Arg Gly Gly Ser Arg Asp Asp Asp Asp Pro			
	1045		1050	1055
20	Ile Ala Ile Val Gly Val Gly Cys Arg Leu Pro Gly Gly Val Asp Ser			
	1060		1065	1070
	Arg Ala Ala Leu Trp Glu Leu Leu Glu Ser Gly Ala Asp Ala Ile Ser			
	1075		1080	1085
25	Ser Phe Pro Thr Asp Arg Gly Trp Asp Leu Asp Gly Leu Tyr Asp Pro			
	1090		1095	1100
	Glu Pro Gly Thr Pro Gly Lys Thr Tyr Val Arg Glu Gly Gly Phe Leu			
	1105		1110	1115
	1120			
30	His Ser Ala Ala Glu Phe Asp Ala Glu Phe Phe Gly Ile Ser Pro Arg			
	1125		1130	1135
	Glu Ala Thr Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Ala Ser			
35	1140		1145	1150
	Trp Glu Ala Leu Glu Asp Ala Gly Val Leu Pro Glu Ser Leu Arg Gly			
	1155		1160	1165
40	Gly Asp Ala Gly Val Phe Val Gly Ala Thr Ala Pro Glu Tyr Gly Pro			
	1170		1175	1180
	Arg Leu His Glu Gly Ala Asp Gly Tyr Glu Gly Tyr Leu Leu Thr Gly			
	1185		1190	1195
	1200			
45	Thr Thr Ala Ser Val Ala Ser Gly Arg Ile Ala Tyr Thr Leu Gly Thr			
	1205		1210	1215
	Gly Gly Pro Ala Leu Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val			
	1220		1225	1230
50	Ala Leu His Leu Ala Val Gln Ala Leu Arg Arg Gly Glu Cys Gly Leu			
	1235		1240	1245
	Ala Leu Ala Gly Gly Ala Thr Val Met Ser Gly Pro Gly Met Phe Val			
	1250		1255	1260
55	Glu Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg Cys Met Pro			

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	1265	1270	1275	1280
	Phe Ser Ala Asp Ala Asp Gly Thr Ala Trp Ser Glu Gly Val Ala Val			
5	1285		1290	1295
	Leu Ala Leu Glu Arg Leu Ser Asp Ala Arg Arg Ala Gly His Arg Val			
	1300	1305		1310
10	Leu Gly Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn			
	1315	1320	1325	
	Gly Leu Thr Ala Pro Asn Arg Ser Ala Gln Glu Gly Val Ile Arg Ala			
15	1330	1335	1340	
	Ala Leu Ala Asp Ala Gly Leu Ala Pro Gly Asp Val Asp Ala Val Glu			
	1345	1350	1355	1360
	Ala His Gly Thr Gly Thr Ala Leu Gly Asp Pro Ile Glu Ala Ser Ala			
	1365	1370		1375
20	Leu Leu Ala Thr Tyr Gly Arg Glu Arg Val Gly Asp Pro Leu Trp Leu			
	1380	1385	1390	
	Gly Ser Leu Lys Ser Asn Val Gly His Thr Gln Ala Ala Ala Gly Ala			
	1395	1400	1405	
25	Ala Gly Val Val Lys Met Leu Leu Ala Leu Glu His Gly Thr Leu Pro			
	1410	1415	1420	
	Arg Thr Leu His Ala Asp Arg Pro Ser Thr His Val Asp Trp Ser Ser			
	1425	1430	1435	1440
30	Gly Thr Val Ala Leu Leu Ala Glu Ala Arg Arg Trp Pro Arg Arg Ser			
	1445	1450	1455	
	Asp Arg Pro Arg Arg Ala Ala Val Ser Ser Phe Gly Ile Ser Gly Thr			
35	1460	1465	1470	
	Asn Ala His Leu Ile Ile Glu Glu Ala Pro Glu Trp Val Glu Asp Ile			
	1475	1480	1485	
40	Asp Gly Val Ala Ala Pro Asp Arg Gly Thr Ala Asp Ala Ala Pro			
	1490	1495	1500	
	Ser Pro Leu Leu Leu Ser Ala Arg Ser Glu Gly Ala Leu Arg Ala Gln			
	1505	1510	1515	1520
45	Ala Val Arg Leu Gly Glu Tyr Val Glu Arg Val Gly Ala Asp Pro Arg			
	1525	1530	1535	
	Asp Val Ala Tyr Ser Leu Ala Ser Thr Arg Thr Leu Phe Glu His Arg			
	1540	1545	1550	
50	Ala Val Val Pro Cys Gly Gly Arg Gly Glu Leu Val Ala Ala Leu Gly			
	1555	1560	1565	
	Gly Phe Ala Ala Gly Arg Val Ser Gly Gly Val Arg Ser Gly Arg Ala			
	1570	1575	1580	
55	Val Pro Gly Gly Val Gly Val Leu Phe Thr Gly Gln Gly Ala Gln Trp			

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	1585	1590	1595	1600
	Val Gly Met Gly Arg Gly Leu Tyr Ala Gly	Gly Val Phe Ala Glu		
5	1605	1610	1615	
	Val Leu Asp Glu Val Leu Ser Met Val Gly	Glu Val Asp Gly Arg Ser		
	1620	1625	1630	
10	Leu Arg Asp Val Met Phe Gly Asp Val Asp	Val Asp Ala Gly		
	1635	1640	1645	
	Ala Asp Ala Gly Ala Gly Ala Gly Val	Gly Ser Gly Ser Gly		
	1650	1655	1660	
15	Ser Val Gly Gly Leu Leu Gly Arg Thr Glu	Phe Ala Gln Pro Ala Leu		
	1665	1670	1675	1680
	Phe Ala Leu Glu Val Ala Leu Phe Arg Ala	Leu Glu Ala Arg Gly Val		
	1685	1690	1695	
20	Glu Val Ser Val Val Leu Gly His Ser Val	Gly Glu Val Ala Ala Ala		
	1700	1705	1710	
	Tyr Val Ala Gly Val Leu Ser Leu Gly Asp	Ala Val Arg Leu Val Val		
	1715	1720	1725	
25	Ala Arg Gly Gly Leu Met Gly Gly Leu Pro	Val Gly Gly Met Trp		
	1730	1735	1740	
	Ser Val Gly Ala Ser Glu Ser Val Val Arg	Gly Val Val Glu Gly Leu		
	1745	1750	1755	1760
30	Gly Glu Trp Val Ser Val Ala Ala Val Asn	Gly Pro Arg Ser Val Val		
	1765	1770	1775	
	Leu Ser Gly Asp Val Gly Val Leu Glu Ser Val Val Ala	Ser Leu Met		
35	1780	1785	1790	
	Gly Asp Gly Val Glu Cys Arg Arg Leu Asp Val Ser	His Gly Phe His		
	1795	1800	1805	
40	Ser Val Leu Met Glu Pro Val Leu Gly Glu Phe Arg	Gly Val Val Glu		
	1810	1815	1820	
	Ser Leu Glu Phe Gly Arg Val Arg Pro Gly Val Val Val	Ser Gly		
	1825	1830	1835	1840
45	Val Ser Gly Gly Val Val Gly Ser Gly Glu Leu	Gly Asp Pro Gly Tyr		
	1845	1850	1855	
	Trp Val Arg His Ala Arg Glu Ala Val Arg Phe	Ala Asp Gly Val Gly		
	1860	1865	1870	
50	Val Val Arg Gly Leu Gly Val Gly Thr Leu Val	Glu Val Gly Pro His		
	1875	1880	1885	
	Gly Val Leu Thr Gly Met Ala Gly Glu Cys Leu	Gly Ala Gly Asp Asp		
	1890	1895	1900	
55	Val Val Val Val Pro Ala Met Arg Arg Gly	Arg Ala Glu Arg Glu Val		

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	1905	1910	1915	1920
	Phe Glu Ala Ala Leu Ala Thr Val Phe Thr Arg Asp Ala Gly Leu Asp			
5	1925		1930	1935
	Ala Thr Ala Leu His Thr Gly Ser Thr Gly Arg Arg Ile Asp Leu Pro			
	1940	1945		1950
10	Thr Tyr Pro Phe Gln Arg Asp Arg Tyr Trp Leu Asp Pro Val Arg Thr			
	1955	1960	1965	
	Ala Val Thr Gly Val Glu Pro Ala Gly Ser Pro Ala Asp Ala Arg Ala			
	1970	1975	1980	
15	Thr Glu Arg Gly Arg Ser Thr Thr Ala Gly Ile Arg Tyr Arg Val Ala			
	1985	1990	1995	2000
	Trp Gln Pro Ala Val Val Asp Arg Gly Asn Pro Gly Pro Ala Gly His			
	2005	2010	2015	
20	Val Leu Leu Leu Ala Pro Asp Glu Asp Thr Ala Asp Ser Gly Leu Ala			
	2020	2025	2030	
	Pro Ala Ile Ala Arg Glu Leu Ala Val Arg Gly Ala Glu Val His Thr			
	2035	2040	2045	
25	Val Ala Val Pro Val Gly Thr Gly Arg Glu Ala Ala Gly Asp Leu Leu			
	2050	2055	2060	
	Arg Ala Ala Gly Asp Gly Ala Ala Arg Ser Thr Arg Val Leu Trp Leu			
	2065	2070	2075	2080
30	Ala Pro Ala Glu Pro Asp Ala Ala Asp Ala Val Ala Leu Val Gln Ala			
	2085	2090	2095	
	Leu Gly Glu Ala Val Pro Glu Ala Pro Leu Trp Ile Thr Thr Arg Glu			
	2100	2105	2110	
35	Ala Ala Ala Val Arg Pro Asp Glu Thr Pro Ser Val Gly Gly Ala Gln			
	2115	2120	2125	
	Leu Trp Gly Leu Gly Gln Val Ala Ala Leu Glu Leu Gly Arg Arg Trp			
40	2130	2135	2140	
	Gly Gly Leu Ala Asp Leu Pro Gly Ser Ala Ser Pro Ala Val Leu Arg			
	2145	2150	2155	2160
	Thr Phe Val Gly Ala Leu Leu Ala Gly Gly Glu Asn Gln Phe Ala Val			
45	2165	2170	2175	
	Arg Pro Ser Gly Val His Val Arg Arg Val Val Pro Ala Pro Val Pro			
	2180	2185	2190	
50	Val Pro Ala Ser Ala Arg Thr Val Thr Thr Ala Pro Ala Thr Ala Val			
	2195	2200	2205	
	Gly Glu Asp Ala Arg Asn Asp Thr Ser Asp Val Val Val Pro Asp Asp			
	2210	2215	2220	
55	Arg Trp Ser Ser Gly Thr Val Leu Ile Thr Gly Gly Thr Gly Ala Leu			

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	2225	2230	2235	2240
	Gly Ala Gln Val Ala Arg Arg Leu Ala Arg Ser Gly Ala Ala Arg Leu			
5	2245	2250	2255	
	Leu Leu Val Gly Arg Arg Gly Ala Ala Gly Pro Gly Val Gly Glu Leu			
	2260	2265	2270	
10	Val Glu Glu Leu Thr Ala Leu Gly Ser Glu Val Ala Val Glu Ala Cys			
	2275	2280	2285	
	Asp Val Ala Asp Arg Asp Ala Leu Ala Ala Leu Leu Ala Gly Leu Pro			
	2290	2295	2300	
15	Glu Glu Arg Pro Leu Val Ala Val Leu His Ala Ala Gly Val Leu Asp			
	2305	2310	2315	2320
	Asp Gly Val Leu Asp Ser Leu Thr Ser Asp Arg Val Asp Ala Val Leu			
	2325	2330	2335	
20	Arg Asp Lys Val Thr Ala Ala Arg His Leu Asp Glu Leu Thr Ala Asp			
	2340	2345	2350	
	Leu Pro Leu Asp Ala Phe Val Leu Phe Ser Ser Ile Val Gly Val Trp			
	2355	2360	2365	
25	Gly Asn Gly Gly Gln Ala Val Tyr Ala Ala Ala Asn Ala Ala Leu Asp			
	2370	2375	2380	
	Ala Leu Ala Gln Arg Arg Ala Arg Gly Ala Arg Ala Ala Ser Ile			
	2385	2390	2395	2400
30	Ala Trp Gly Pro Trp Ala Gly Ala Gly Met Ala Ser Gly Thr Ala Ala			
	2405	2410	2415	
	Lys Ser Phe Glu Arg Asp Gly Val Thr Ala Leu Asp Pro Glu Arg Ala			
	2420	2425	2430	
35	Leu Asp Val Leu Asp Asp Val Val Gly Ala Gly Gly Thr Ser Ala Ala			
	2435	2440	2445	
	Gly Thr His Ala Ala Gly Glu Ser Ser Leu Leu Val Ala Asp Val Asp			
40	2450	2455	2460	
	Trp Glu Thr Phe Val Gly Arg Ser Val Thr Arg Arg Thr Trp Ser Leu			
	2465	2470	2475	2480
45	Phe Asp Gly Val Ser Ala Ala Arg Ser Ala Arg Ala Gly His Ala Ala			
	2485	2490	2495	
	Asp Asp Arg Ala Ala Leu Thr Pro Gly Thr Arg Pro Gly Asp Gly Ala			
	2500	2505	2510	
50	Pro Gly Ser Gly Gln Asp Gly Gly Glu Gly Arg Pro Trp Leu Ser			
	2515	2520	2525	
	Val Gly Pro Ser Pro Ala Glu Arg Arg Ala Leu Leu Thr Leu Val			
	2530	2535	2540	
55	Arg Ser Glu Ala Ala Gly Ile Leu Arg His Ala Ser Ala Asp Ala Val			

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	2545	2550	2555	2560
	Asp Pro Glu Leu Ala Phe Arg Ser Ala Gly Phe Asp Ser Leu Thr Val			
5	2565	2570	2575	
	Leu Glu Leu Arg Asn Arg Leu Thr Ala Ala Thr Gly Leu Asn Leu Pro			
	2580	2585	2590	
10	Asn Thr Leu Leu Phe Asp His Pro Thr Pro Leu Ser Leu Ala Ser His			
	2595	2600	2605	
	Leu His Asp Glu Leu Phe Gly Pro Asp Ser Glu Ala Glu Pro Ala Ala			
15	2610	2615	2620	
	Ala Ala Pro Thr Pro Val Met Ala Asp Glu Arg Glu Pro Ile Ala Ile			
	2625	2630	2635	2640
	Val Gly Met Ala Cys Arg Tyr Pro Gly Gly Val Ala Ser Pro Asp Asp			
	2645	2650	2655	
20	Leu Trp Asp Leu Val Ala Gly Asp Gly His Thr Leu Ser Pro Phe Pro			
	2660	2665	2670	
	Ala Asp Arg Gly Trp Asp Val Glu Gly Leu Tyr Asp Pro Glu Pro Gly			
	2675	2680	2685	
25	Val Pro Gly Lys Ser Tyr Val Arg Glu Gly Phe Leu Arg Ser Ala			
	2690	2695	2700	
	Ala Glu Phe Asp Ala Glu Phe Gly Ile Ser Pro Arg Glu Ala Thr			
	2705	2710	2715	2720
30	Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr Ser Trp Glu Ala			
	2725	2730	2735	
	Leu Glu Arg Ala Gly Ile Val Pro Asp Ser Leu Arg Gly Thr Arg Thr			
35	2740	2745	2750	
	Gly Val Phe Ser Gly Ile Ser Gln Gln Asp Tyr Ala Thr Gln Leu Gly			
	2755	2760	2765	
40	Asp Ala Ala Asp Thr Tyr Gly Gly His Val Leu Thr Gly Thr Leu Gly			
	2770	2775	2780	
	Ser Val Ile Ser Gly Arg Val Ala Tyr Ala Leu Gly Leu Glu Gly Pro			
	2785	2790	2795	2800
45	Ala Leu Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His			
	2805	2810	2815	
	Leu Ala Val Gln Ser Leu Arg Arg Gly Glu Cys Asp Leu Ala Leu Ala			
	2820	2825	2830	
50	Gly Gly Val Thr Val Met Ala Thr Pro Thr Val Phe Val Glu Phe Ser			
	2835	2840	2845	
	Arg Gln Arg Gly Leu Ala Ala Asp Gly Arg Cys Lys Ala Phe Ala Glu			
	2850	2855	2860	
55	Gly Ala Asp Gly Thr Ala Trp Ala Glu Gly Val Gly Val Leu Leu Val			

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	2865	2870	2875	2880
	Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly His Arg Val Leu Ala Val			
5	2885	2890	2895	
	Val Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr			
	2900	2905	2910	
10	Ala Pro Ser Gly Pro Ala Gln Gln Arg Val Ile Arg Glu Ala Leu Ala			
	2915	2920	2925	
	Asp Ala Gly Leu Val Pro Ala Asp Val Asp Val Val Glu Ala His Gly			
	2930	2935	2940	
15	Thr Gly Thr Ala Leu Gly Asp Pro Ile Glu Ala Gly Ala Leu Leu Ala			
	2945	2950	2955	2960
	Thr Tyr Gly Arg Glu Arg Val Gly Asp Pro Leu Trp Leu Gly Ser Leu			
	2965	2970	2975	
20	Lys Ser Asn Ile Gly His Ala Gln Ala Ala Ala Gly Val Gly Gly Val			
	2980	2985	2990	
	Ile Lys Val Val Gln Gly Met Arg His Gly Ser Leu Pro Arg Thr Leu			
	2995	3000	3005	
25	His Val Asp Ala Pro Ser Ser Lys Val Glu Trp Ala Ser Gly Ala Val			
	3010	3015	3020	
	Glu Leu Leu Thr Glu Thr Arg Ser Trp Pro Arg Arg Val Glu Arg Val			
	3025	3030	3035	3040
30	Arg Arg Ala Ala Val Ser Ala Phe Gly Val Ser Gly Thr Asn Ala His			
	3045	3050	3055	
	Val Val Leu Glu Glu Ala Pro Ala Glu Ala Gly Ser Glu His Gly Asp			
35	3060	3065	3070	
	Gly Pro Glu Pro Glu Arg Pro Asp Ala Val Thr Gly Pro Leu Ser Trp			
	3075	3080	3085	
40	Val Leu Ser Ala Arg Ser Glu Gly Ala Leu Arg Ala Gln Ala Val Arg			
	3090	3095	3100	
	Leu Arg Glu Cys Val Glu Arg Val Gly Ala Asp Pro Arg Asp Val Ala			
	3105	3110	3115	3120
45	Gly Ser Leu Val Val Ser Arg Ala Ser Phe Gly Glu Arg Ala Val Val			
	3125	3130	3135	
	Val Gly Arg Gly Arg Glu Glu Leu Leu Ala Gly Leu Asp Val Val Ala			
	3140	3145	3150	
50	Ala Gly Ala Pro Val Gly Val Ser Ser Gly Ala Gly Ala Val Val Arg			
	3155	3160	3165	
	Gly Ser Ala Val Arg Gly Arg Gly Val Gly Val Leu Phe Thr Gly Gln			
	3170	3175	3180	
55	Gly Ala Gln Trp Val Gly Met Gly Arg Gly Leu Tyr Ala Gly Gly			

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	3185	3190	3195	3200
	Val Phe Ala Glu Val Leu Asp Glu Val	Leu Ser Val Val Gly Glu Val		
5	3205	3210	3215	
	Asp Gly Arg Ser Leu Arg Asp Val Met Phe Ala Asp Ala Asp Ser Val			
	3220	3225	3230	
10	Leu Gly Gly Leu Leu Gly Arg Thr Glu Phe Ala Gln Pro Ala Leu Phe			
	3235	3240	3245	
	Ala Leu Glu Val Ala Leu Phe Arg Ala Leu Glu Ala Arg Gly Val Glu			
	3250	3255	3260	
15	Val Ser Val Val Leu Gly His Ser Val Gly Glu Val Ala Ala Ala Tyr			
	3265	3270	3275	3280
	Val Ala Gly Val Leu Ser Leu Gly Asp Ala Val Arg Leu Val Val Ala			
	3285	3290	3295	
20	Arg Gly Gly Leu Met Gly Gly Leu Pro Val Gly Gly Met Trp Ser			
	3300	3305	3310	
	Val Gly Ala Ser Glu Ser Val Val Arg Gly Val Val Glu Gly Leu Gly			
	3315	3320	3325	
25	Glu Trp Val Ser Val Ala Ala Val Asn Gly Pro Arg Ser Val Val Leu			
	3330	3335	3340	
	Ser Gly Asp Val Gly Val Leu Glu Ser Val Val Val Thr Leu Met Gly			
	3345	3350	3355	3360
30	Asp Gly Val Glu Cys Arg Arg Leu Asp Val Ser His Gly Phe His Ser			
	3365	3370	3375	
	Val Leu Met Glu Pro Val Leu Gly Glu Phe Arg Gly Val Val Glu Ser			
	3380	3385	3390	
35	Leu Glu Phe Gly Arg Val Arg Pro Gly Val Val Val Ser Gly Val			
	3395	3400	3405	
	Ser Gly Gly Val Val Gly Ser Gly Glu Leu Gly Asp Pro Gly Tyr Trp			
40	3410	3415	3420	
	Val Arg His Ala Arg Glu Ala Val Arg Phe Ala Asp Gly Val Gly Val			
	3425	3430	3435	3440
45	Val Arg Gly Leu Gly Val Gly Thr Leu Val Glu Val Gly Pro His Gly			
	3445	3450	3455	
	Val Leu Thr Gly Met Ala Gly Gln Cys Leu Glu Ala Gly Asp Asp Val			
	3460	3465	3470	
50	Val Val Val Pro Ala Met Arg Arg Gly Arg Pro Glu Arg Glu Val Phe			
	3475	3480	3485	
	Glu Ala Ala Leu Ala Thr Val Phe Thr Arg Asp Ala Gly Leu Asp Ala			
	3490	3495	3500	
55	Thr Thr Leu His Thr Gly Ser Thr Gly Arg Arg Ile Asp Leu Pro Thr			

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	3505	3510	3515	3520
	Tyr Pro Phe Gln His Asn Arg Tyr Trp Ala Thr Gly Ser Val Thr Gly			
5	3525	3530	3535	
	Ala Thr Gly Thr Ser Ala Ala Ala Arg Phe Gly Leu Glu Trp Lys Asp			
	3540	3545	3550	
10	His Pro Phe Leu Ser Gly Ala Thr Pro Ile Ala Gly Ser Gly Ala Leu			
	3555	3560	3565	
	Leu Leu Thr Gly Arg Val Gly Leu Ala Ala His Pro Trp Leu Ala Asp			
	3570	3575	3580	
15	His Ala Ile Ser Gly Thr Val Leu Leu Pro Gly Thr Ala Ile Ala Asp			
	3585	3590	3595	3600
	Leu Leu Leu Arg Ala Val Glu Glu Val Gly Ala Gly Gly Val Glu Glu			
	3605	3610	3615	
20	Leu Thr Leu His Glu Pro Leu Leu Leu Pro Glu Arg Gly Gly Leu His			
	3620	3625	3630	
	Val Gln Val Leu Val Glu Ala Ala Asp Glu Gln Gly Arg Arg Ala Val			
	3635	3640	3645	
25	Ala Val Ala Ala Arg Pro Glu Gly Pro Gly Arg Asp Gly Glu Glu Gln			
	3650	3655	3660	
	Glu Trp Thr Arg His Ala Glu Gly Val Leu Thr Ser Thr Glu Thr Ala			
	3665	3670	3675	3680
30	Val Pro Asp Met Gly Trp Ala Ala Gly Ala Trp Pro Pro Pro Gly Ala			
	3685	3690	3695	
	Glu Pro Ile Asp Val Glu Glu Leu Tyr Asp Ala Phe Ala Ala Asp Gly			
	3700	3705	3710	
35	Tyr Gly Tyr Gly Pro Ala Phe Thr Ala Leu Ser Gly Val Trp Arg Leu			
	3715	3720	3725	
	Gly Asp Glu Leu Phe Ala Glu Val Arg Arg Pro Ala Gly Gly Ala Gly			
40	3730	3735	3740	
	Thr Thr Gly Asp Gly Phe Gly Val His Pro Ala Leu Phe Asp Ala Ala			
	3745	3750	3755	3760
45	Leu His Pro Trp Arg Ala Gly Gly Leu Leu Pro Asp Thr Gly Gly Thr			
	3765	3770	3775	
	Thr Trp Ala Pro Phe Ser Trp Gln Gly Ile Ala Leu His Thr Thr Gly			
	3780	3785	3790	
50	Ala Glu Thr Leu Arg Val Arg Leu Ala Pro Ala Ala Gly Gly Thr Glu			
	3795	3800	3805	
	Ser Ala Phe Ser Val Gln Ala Ala Asp Pro Ala Gly Thr Pro Val Leu			
	3810	3815	3820	
55	Thr Leu Asp Ala Leu Leu Leu Arg Pro Val Thr Leu Gly Arg Ala Asp			

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	3825	3830	3835	3840
	Ala Pro Gln Pro Leu Tyr Arg Val Asp Trp Gln Pro Val Gly Gln Gly			
5	3845	3850	3855	
	Thr Glu Ala Ser Gly Ala Gln Gly Trp Thr Val Leu Gly Gln Ala Ala			
	3860	3865	3870	
10	Ala Glu Thr Val Ala Gln Pro Ala Ala His Ala Asp Leu Thr Ala Leu			
	3875	3880	3885	
	Arg Thr Ala Val Ala Ala Gly Thr Pro Val Pro Arg Leu Val Val			
	3890	3895	3900	
15	Val Ser Pro Val Asp Thr Arg Leu Asp Glu Gly Pro Val Leu Ala Asp			
	3905	3910	3915	3920
	Ala Glu Ala Arg Ala Arg Ala Gly Asp Gly Trp Asp Asp Asp Pro Leu			
	3925	3930	3935	
20	Arg Val Ala Leu Gly Arg Gly Leu Thr Leu Val Arg Glu Trp Val Glu			
	3940	3945	3950	
	Asp Glu Arg Leu Ala Asp Ser Arg Leu Val Val Leu Thr Arg Gly Ala			
	3955	3960	3965	
25	Val Ala Ala Gly Pro Gly Asp Val Pro Asp Leu Thr Gly Ala Ala Leu			
	3970	3975	3980	
	Trp Gly Leu Leu Arg Ser Ala Gln Ser Glu Tyr Pro Asp Arg Phe Thr			
	3985	3990	3995	4000
30	Leu Ile Asp Val Asp Asp Ser Pro Glu Ser Arg Ala Ala Leu Pro Arg			
	4005	4010	4015	
	Ala Leu Gly Ser Ala Glu Arg Gln Leu Ala Leu Arg Thr Gly Asp Val			
	4020	4025	4030	
35	Leu Ala Pro Ala Leu Val Pro Met Ala Thr Arg Pro Ala Glu Thr Thr			
	4035	4040	4045	
	Pro Ala Thr Ala Val Ala Ser Ala Thr Thr Gln Thr Gln Val Thr Ala			
40	4050	4055	4060	
	Pro Ala Pro Asp Asp Pro Ala Ala Asp Ala Val Phe Asp Pro Ala Gly			
	4065	4070	4075	4080
45	Thr Val Leu Ile Thr Gly Gly Thr Gly Ala Leu Gly Arg Arg Val Ala			
	4085	4090	4095	
	Ser His Leu Ala Arg Arg Tyr Gly Val Arg His Met Leu Leu Val Ser			
	4100	4105	4110	
50	Arg Arg Gly Pro Asp Ala Pro Glu Ala Gly Pro Leu Glu Arg Glu Leu			
	4115	4120	4125	
	Ala Gly Leu Gly Val Thr Ala Thr Phe Leu Ala Cys Asp Leu Thr Asp			
	4130	4135	4140	
55	Ile Glu Ala Val Arg Lys Ala Val Ala Val Pro Ser Asp His Pro			

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4145	4150	4155	4160
Leu Thr Gly Val Val His Thr Ala Gly Val Leu Asp Asp Gly Ala Leu			
5	4165	4170	4175
Thr Gly Leu Thr Arg Gln Arg Leu Asp Thr Val Leu Arg Pro Lys Ala			
	4180	4185	4190
10	Asp Ala Val Arg Asn Leu His Glu Ala Thr Leu Asp Arg Pro Leu Arg		
	4195	4200	4205
Ala Phe Val Leu Phe Ser Ala Ala Ala Gly Leu Leu Gly Arg Pro Gly			
15	4210	4215	4220
Gln Ala Ser Tyr Ala Ala Asn Ala Val Leu Asp Ala Leu Ala Gly			
	4225	4230	4235
Ala Arg Arg Ala Ala Gly Leu Pro Ala Val Ser Leu Ala Trp Gly Leu			
	4245	4250	4255
20	Trp Asp Glu Gln Thr Gly Met Ala Gly Gly Leu Asp Glu Met Ala Leu		
	4260	4265	4270
Arg Val Leu Arg Arg Asp Gly Ile Ala Ala Met Pro Pro Glu Gln Gly			
25	4275	4280	4285
Leu Glu Leu Leu Asp Leu Ala Leu Thr Gly His Arg Asp Gly Pro Ala			
	4290	4295	4300
30			
35			
40			
45			
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Val Leu Val Pro Leu Leu Leu Asp Gly Ala Ala Leu Arg Arg Thr Ala
 4305 4310 4315 4320
 5 Lys Glu Arg Gly Ala Ala Thr Met Ser Pro Leu Leu Arg Ala Leu Leu
 4325 4330 4335
 Pro Ala Ala Leu Arg Arg Ser Gly Gly Ala Gly Ala Pro Ala Ala Ala
 4340 4345 4350
 10 Asp Arg His Gly Lys Glu Ala Asp Pro Gly Ala Gly Arg Leu Ala Gly
 4355 4360 4365
 Met Val Ala Leu Glu Ala Ala Glu Arg Ser Ala Ala Val Leu Glu Leu
 4370 4375 4380
 15 Val Thr Glu Gln Val Ala Glu Val Leu Gly Tyr Ala Ser Ala Ala Glu
 4385 4390 4395 4400
 Ile Glu Pro Glu Arg Pro Phe Arg Glu Ile Gly Val Asp Ser Leu Ala
 20 4405 4410 4415
 Ala Val Glu Leu Arg Asn Arg Leu Ser Arg Leu Val Gly Leu Arg Leu
 4420 4425 4430
 25 Pro Thr Thr Leu Ser Phe Asp His Pro Thr Pro Lys Asp Met Ala Gln
 4435 4440 4445
 His Ile Asp Gly Gln Leu Pro Arg Pro Ala Gly Ala Ser Pro Ala Asp
 4450 4455 4460
 30 Ala Ala Leu Glu Gly Ile Gly Asp Leu Ala Arg Ala Val Ala Leu Leu
 4465 4470 4475 4480
 Gly Thr Gly Asp Ala Arg Arg Ala Glu Val Arg Glu Gln Leu Val Gly
 4485 4490 4495
 35 Leu Leu Ala Ala Leu Asp Pro Pro Gly Arg Thr Gly Thr Ala Ala Pro
 4500 4505 4510
 Gly Val Pro Ser Gly Ala Asp Gly Ala Glu Pro Thr Val Thr Asp Arg
 4515 4520 4525
 40 Leu Asp Glu Ala Thr Asp Asp Glu Ile Phe Ala Phe Leu Asp Glu Gln
 4530 4535 4540
 45 Leu *
 4545

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(2) INFORMATION FOR SEQ ID NO:15:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGAGGCCGGC GGGCC

Claims

- 20 1. A DNA molecule comprising an isolated DNA sequence that encodes a tylactone synthase domain.
2. The DNA molecule as claimed in Claim 1 wherein the isolated DNA sequence is selected from the group consisting of:
nucleotides 942 to 2156, 2571 to 3557, 3675 to 3929, 3993 to 5264, 5631 to 6617, 7410 to 7949, 8220 to
25 8471, 8541 to 9812, 10260 to 11246, 11319 to 11876, 12861 to 13415, 13719 to 13970, 14411 to 15697, 16055
to 17122, 17198 to 17794, 18584 to 19138, 19415 to 19666, 20136 to 21404, 21771 to 22757, 23541 to 24077,
24360 to 24611, 24675 to 25949, 26292 to 27284, 27360 to 27917, 28767 to 29813, 29829 to 30368, 30651 to
30 30902, 31337 to 32608, 32975 to 33961, 34694 to 35236, 35492 to 35743, 36360 to 37631, 37989 to 38987,
39759 to 40313, 40575 to 40826, and 41235 to 41333 all in SEQ ID NO:1.
- 35 3. The DNA molecule as claimed in Claim 1 wherein the isolated DNA sequence is selected from the group consisting of:
nucleotides 942 to 8471, 8541 to 13970, 14411 to 19666, 20136 to 24611, 24675 to 30902, 31337 to 35743,
and 36360 to 40826 all in SEQ ID NO:1.
- 40 4. The DNA molecule as claimed in Claim 1 wherein the isolated DNA sequence is selected from the group consisting of:
nucleotides 816 to 14234, 14351 to 19945, 20010 to 31199, 31232 to 36067, and 36249 to 41774 all in SEQ
ID NO:1.
5. The DNA molecule as claimed in Claim 1 wherein the isolated DNA sequence is SEQ ID NO:1.
6. A polypeptide comprising an amino acid sequence that consists of a tylactone synthase domain.
- 45 7. The polypeptide of claim 6 wherein the amino acid sequence is selected from the group consisting of:
(a) amino acids 43 to 447, 586 to 914, 954 to 1038, 1060 to 1483, 1606 to 1934, 2199 to 2378, 2469 to 2552,
2576 to 2999, 3149 to 3477, 3502 to 3687, 4016 to 4200, and 4302 to 4385 in SEQ ID NO:2;
50 (b) amino acids 21 to 449, 569 to 924, 950 to 1148, 1412 to 1596, and 1689 to 1772 in SEQ ID NO:3;
(c) amino acids 43 to 465, 588 to 916, 1178 to 1356, and 1451 to 1534, 1556 to 1980, 2095 to 2425, 2451 to
2636, 3274 to 3453, and 3548 to 3631 in SEQ ID NO:4;
(d) amino acids 36 to 459, 582 to 910, 1155 to 1335, and 1421 to 1504 in SEQ ID NO:5; and
(e) amino acids 38 to 461, 581 to 913, 1171 to 1355, 1443 to 1526, and 1663 to 1695 in SEQ ID NO:6.
- 55 8. The polypeptide of claim 6 wherein the amino acid sequence is selected from the group consisting of:
(a) amino acids 1060 to 2552 and 2576 to 4385 in SEQ ID NO:2;
(b) amino acids 21 to 1772 in SEQ ID NO:3;

(c) amino acids 43 to 1534 and 1556 to 3631 in SEQ ID NO:4;
(d) amino acids 36 to 1504 in SEQ ID NO:5; and
(e) amino acids 38 to 1526 in SEQ ID NO:6.

5 **9.** The polypeptide of claim 6 wherein the amino acid sequence is selected from the group consisting of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6.

10. A recombinant DNA vector comprising a DNA molecule of Claim 1.

11. A recombinant DNA vector comprising a DNA molecule of Claim 2.

12. A recombinant DNA vector comprising a DNA molecule of Claim 3.

13. A recombinant DNA vector comprising a DNA molecule of Claim 4.

14. A recombinant DNA vector comprising a DNA molecule of Claim 5.

15. A recombinant DNA vector of Claim 10 which is NRRL B-18688.

20. **16.** A recombinant DNA vector of Claim 10 which is NRRL B-18689

17. A host cell transformed with a recombinant DNA vector of Claim 10.

18. A host cell transformed with a recombinant DNA vector of Claim 11.

25. **19.** A host cell transformed with a recombinant DNA vector of Claim 12.

20. A host cell transformed with a recombinant DNA vector of Claim 13.

30. **21.** A host cell transformed with a recombinant DNA vector of Claim 14.

22. The DNA molecule as claimed in Claim 1 wherein the isolated DNA sequence is SEQ ID NO:7.

35. **23.** The polypeptide of SEQ ID NO:8.

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Fig. 1

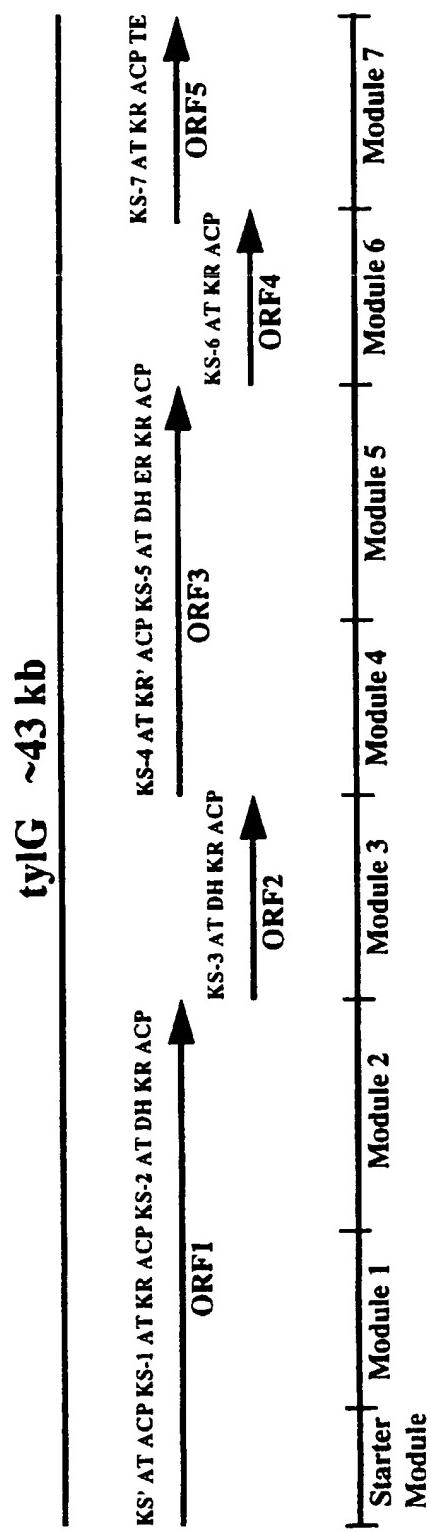


Fig. 2

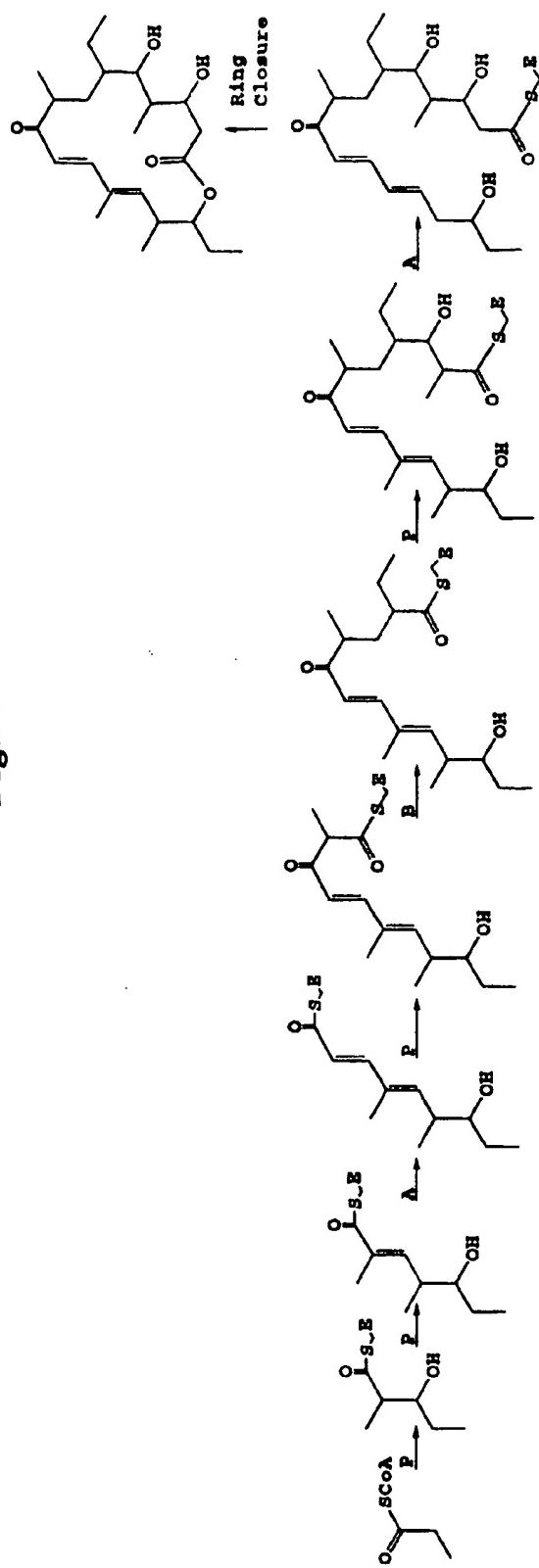


Fig. 3

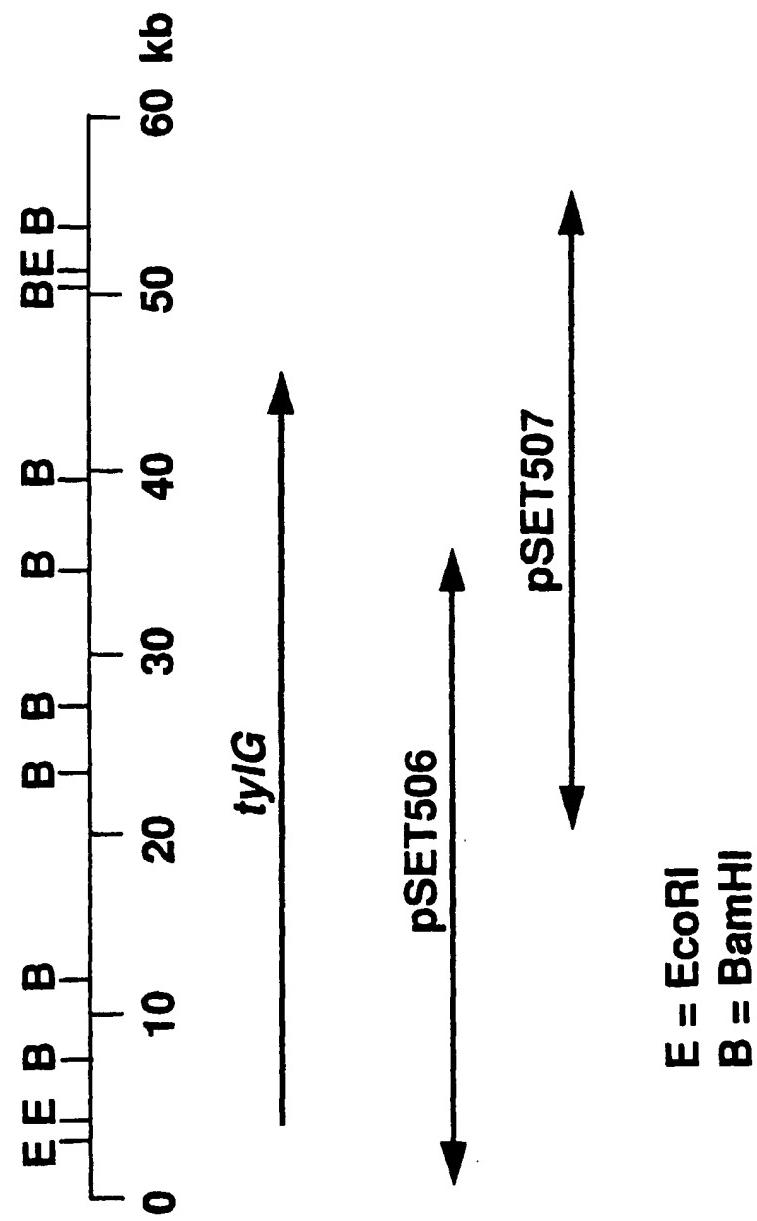
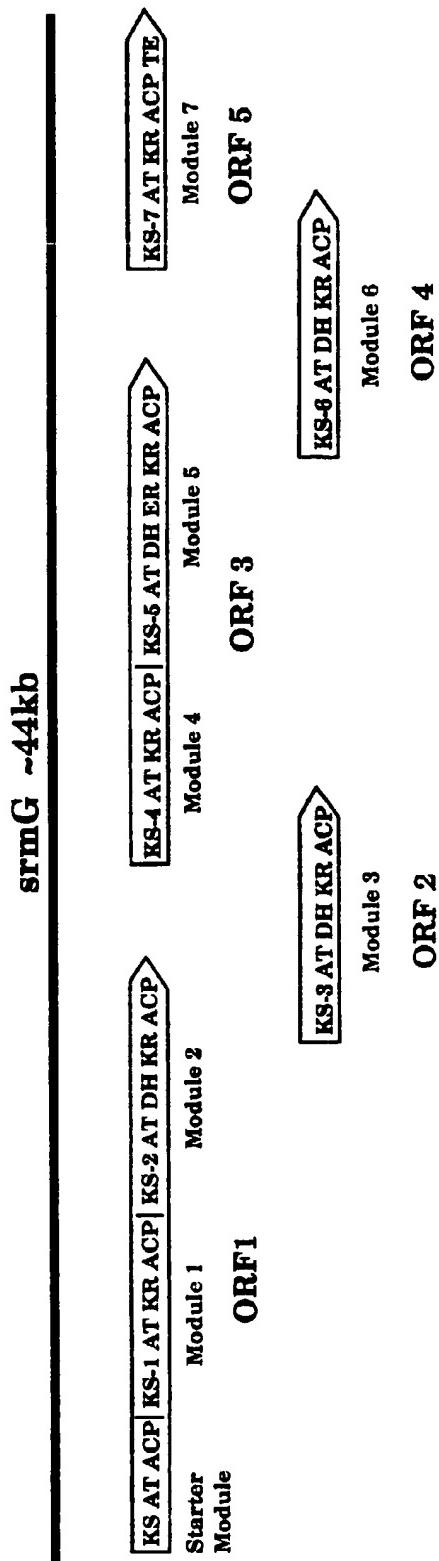


Fig. 4



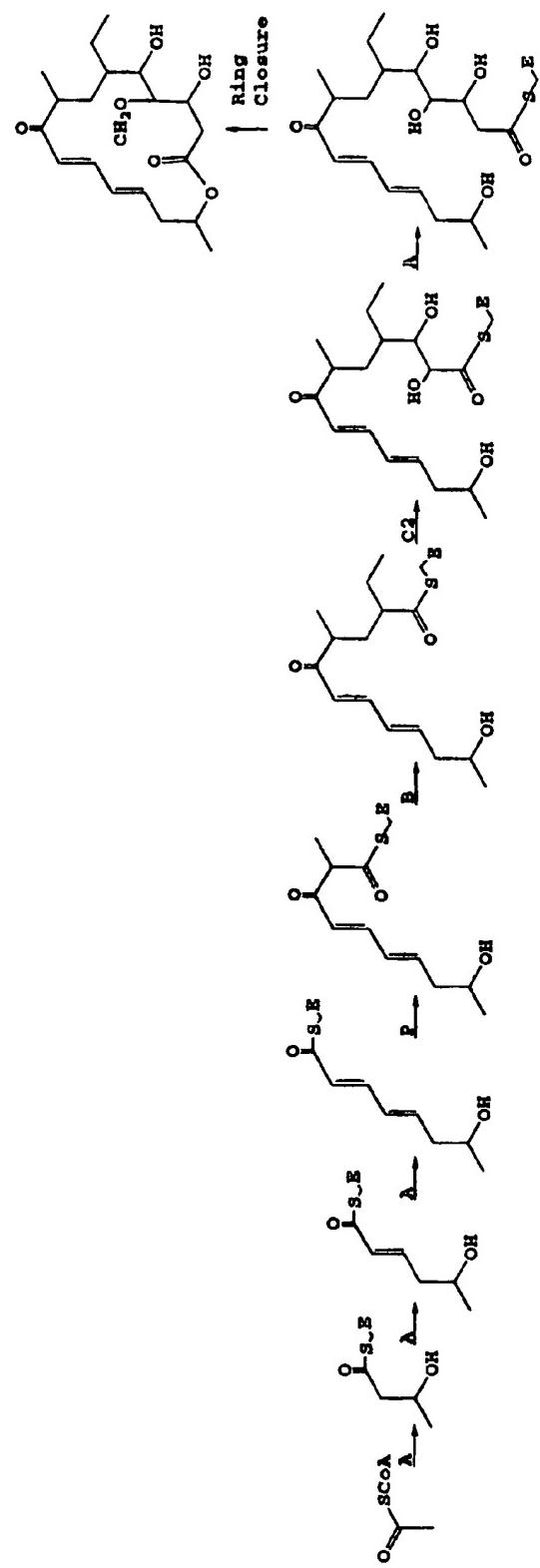
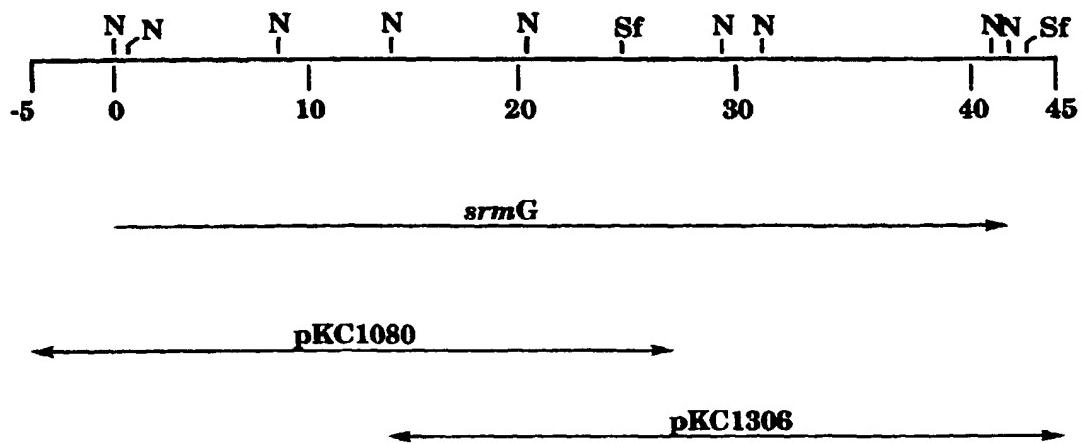


Fig. 5

Fig. 6



N = *Nru*I

Sf = *Sfu*I